

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 18, 2004, 19:17:05 ; Search time 60 Seconds  
(without alignments)  
1290.300 Million cell updates/sec

Title: US-09-819-371-5  
Perfect score: 1496  
Sequence: 1 GSHSLRYSTAVSRGRGEP.....QRYTCHVQHGLOPFLILRW 274

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_29Jan04:\*  
1: Geneseq1980s:\*  
2: Geneseq1990s:\*  
3: Geneseq2000s:\*  
4: Geneseq2001s:\*  
5: Geneseq2002s:\*  
6: Geneseq2003as:\*  
7: Geneseq2003bs:\*  
8: Geneseq2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1496	100.0	274	4	AAG64618 Human can
2	1496	100.0	362	4	AAG64617 Human can
3	1496	100.0	362	4	ABBS0296 HLA-Cw ov
4	1491	99.7	677	4	ABG26726 Novel hum
5	1311	87.6	271	3	AAB43986 Human can
6	1248	83.4	274	1	AAP80911 Consensus
7	1228	82.1	362	1	AAP70155 Sequence
8	1227	82.1	337	1	AAP70590 Sequence
9	1224	81.8	369	4	AAR12482 Novel hum
10	1209	80.8	366	2	AAR12465 HLA-C exo
11	1206	80.6	374	2	AAO30733 Breast ca
12	1206	80.6	374	4	AAO30733 Human pol
13	1204.5	80.5	374	4	AAO06772 Human pol
14	1201	80.3	362	2	AAR03142 Sequence
15	1200	80.2	362	7	AD64171 Human Pro
16	1200	80.2	362	7	AD64175 Human Pro
17	1199	80.1	362	2	AAR03144 Sequence
18	1199	80.1	366	2	AAR12466 HLA-C exo
19	1192	79.7	380	4	AAU32883 Novel hum
20	1186	79.3	362	2	AAR12464 HLA-B35 a
21	1184	79.1	326	5	AAU79454 HLA-G rec
22	1184	79.1	338	7	ADD46572 Human Pro
23	1182	79.0	362	2	AAR12463 HLA-Bw53
24	1174.5	78.5	379	5	ABP70087 Human NOV
25	1174.5	78.5	379	7	ADE40254 Human NOV

26	1169	78.1	215	4	AAG64619	Aag64619 Human can
27	1162	77.7	368	4	AAM24017	Aam24017 Human NOV
28	1158	77.4	364	5	ABP70088	Abp70088 Human NOV
29	1154	77.1	365	3	AAV68268	Aay68268 Human leu
30	1154	77.1	365	3	AAV52922	Aay52922 HLA-A2/A2
31	1154	77.1	365	4	AAB58683	Aab58683 HLA-A2/A2
32	1154	77.1	365	4	AAB36874	Aab36874 MHC class
33	1153	77.1	280	4	AAU10225	Aau10225 Human leu
34	1153	77.1	280	6	ABU08672	Abu08672 Human his
35	1153	77.1	412	2	AAW68385	Aaw68385 Chimeric
36	1153	77.1	415	4	AAU10224	Aau10224 Human par
37	1153	77.1	415	6	ABU08671	Abu08671 Human sin
38	1153	77.1	510	6	AAE36053	Aae36053 B2M-atav
39	1151	76.9	365	3	AAV68272	Aay68272 Human leu
40	1151	76.9	365	3	AAV68267	Aay68267 Human leu
41	1151	76.9	365	3	AAV52926	Aay52926 HLA-A2/A2
42	1151	76.9	365	3	AAV52921	Aay52921 HLA-A2/A2
43	1151	76.9	365	4	AAB58682	Aab58682 HLA-A2/A2
44	1151	76.9	365	4	AAB58687	Aab58687 HLA-A2/A2
45	1150	76.9	274	3	AAV68275	Aay68275 Human leu

## ALIGNMENTS

## RESULT 1

AAG64618 standard; protein; 274 AA.  
ID AAG64618 standard; protein; 274 AA.

XX AAG64618;  
XX  
DT 12-SEP-2001 (first entry)  
XX  
DE Human cancer cell specific HLA-F antigen SEQ ID 5.  
XX  
KW HLA-F antigen; cancer cell specific; human.  
XX  
OS Homo sapiens.  
XX  
PN JP2001095584-A.  
XX  
PD 10-APR-2001.  
XX  
PF 30-SEP-1999; 99JP-00279566.  
XX  
PR 30-SEP-1999; 99JP-00279566.  
XX  
PA (EGAW/) EGAWA K.  
PA (MEDI-) MEDINET KK.  
PA (KIMU/) KIMURA K.  
XX  
DR WPI: 2001-360493/38.  
DR N-PSDB; AAH45556.  
XX  
PT Novel cancer cell-specific HLA-F antigen useful for diagnosing cancer.  
XX  
PS Claim 2; page 10-11; 12pp; Japanese.  
XX  
CC This invention relates to a cancer cell specific HLA-F antigen. The invention includes DNA encoding the antigen, and a method for the preparation of the cancer cell specific HLA-F antigen. The antigen may be used in a method to diagnose cancer, in which the protein is used to detect anti-HLA-F antibodies in bodily fluids of the patient. The present sequence represents the cancer cell-specific HLA-F antigen of the invention

XX Sequence 274 AA;

Query Match 100.0%; Score 1496; DB 4; Length 274;  
Best Local Similarity 100.0%; Pred. No. 1.3e-133;  
Matches 274; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSHSLRYSTAVSRGRGEPRIAYVYDDTQFLRFDSDAAIPRMEPREPWYEQSPQYW 60

Db 1 GSHSLRYFSTAVSRPGRGEPYIAVEYDDTQFLRFDSDAAIPRMEPRPFWVEQGPQYW 60  
QY 61 EWTGAKANAQTDRLVALNLLRRYNQSEAGSHTLQMGNGCDMPDGRLLRGYHGHAYDG 120  
Db 61 EWTGAKANAQTDRLVALNLLRRYNQSEAGSHTLQMGNGCDMPDGRLLRGYHGHAYDG 120  
QY 121 KDYSISNEDLSRSTAADTVAQITQRFYEABEYAEFFTYLGECLLELLRRYLENGKETLQ 180  
Db 121 KDYSISNEDLSRSTAADTVAQITQRFYEABEYAEFFTYLGECLLELLRRYLENGKETLQ 180  
QY 181 RADPPKAHVAHPISDHEATLRCWALGFYPAEITLTWQDGEQOTQDTLVEVTRPAGDGT 240  
Db 181 RADPPKAHVAHPISDHEATLRCWALGFYPAEITLTWQDGEQOTQDTLVEVTRPAGDGT 240  
QY 241 FQKWAHVVPVSGEORQYTCVHVEGLPOPLILRW 274  
Db 241 FQKWAHVVPVSGEORQYTCVHVEGLPOPLILRW 274  
RESULT 2  
AAG64617  
ID AAG64617 standard; protein; 362 AA.  
AC AAG64617;  
XX  
XX  
DT 12-SEP-2001 (first entry)  
DE Human cancer cell specific HLA-F antigen SEQ ID 4.  
XX HLA-F antigen; cancer cell specific; human.  
XX Homo sapiens.  
XX JP2001095584-A.  
XX  
XX 10-APR-2001.  
XX 30-SEP-1999; 99JP-00279566.  
XX 30-SEP-1999; 99JP-00279566.  
XX (EGAW//) EGAWA K.  
FA (MEDI-) MEDINET KK.  
FA (KIMU//) KIMURA K.  
XX  
XX WPI; 2001-360493/38.  
XX N-PSDB; AAH45555.  
XX  
XX Novel cancer cell-specific HLA-F antigen useful for diagnosing cancer.  
XX Disclosure; Page 9-10; 12pp; Japanese.  
XX  
XX This invention relates to a cancer cell specific HLA-F antigen. The  
CC invention includes DNA encoding the antigen, and a method for the  
CC preparation of the cancer cell specific HLA-F antigen. The antigen may be  
CC used in a method to diagnose cancer in which the protein is used to  
CC detect anti-HLA-F antibodies in bodily fluids of the patient. The present  
CC invention represents the cancer cell-specific HLA-F antigen of the  
CC invention  
XX  
SQ Sequence 362 AA;  
Query Match 100.0%; Score 1496; DB 4; Length 362;  
Best Local Similarity 100.0%; Pred. No. 1.9e-133;  
Matches 274; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GSHSLRYFSTAVSRPGRGEPYIAVEYDDTQFLRFDSDAAIPRMEPRPFWVEQGPQYW 60  
Db 22 GSHSLRYFSTAVSRPGRGEPYIAVEYDDTQFLRFDSDAAIPRMEPRPFWVEQGPQYW 81  
QY 61 EWTGAKANAQTDRLVALNLLRRYNQSEAGSHTLQMGNGCDMPDGRLLRGYHGHAYDG 120

Db 82 EWTGAKANAQTDRLVALNLLRRYNQSEAGSHTLQMGNGCDMPDGRLLRGYHGHAYDG 141  
QY 121 KDYSISNEDLSRSTAADTVAQITQRFYEABEYAEFFTYLGECLLELLRRYLENGKETLQ 180  
Db 142 KDYSISNEDLSRSTAADTVAQITQRFYEABEYAEFFTYLGECLLELLRRYLENGKETLQ 201  
QY 181 RADPPKAHVAHPISDHEATLRCWALGFYPAEITLTWQDGEQOTQDTLVEVTRPAGDGT 240  
Db 202 RADPPKAHVAHPISDHEATLRCWALGFYPAEITLTWQDGEQOTQDTLVEVTRPAGDGT 261  
QY 241 FQKWAHVVPVSGEORQYTCVHVEGLPOPLILRW 274  
Db 262 FQKWAHVVPVSGEORQYTCVHVEGLPOPLILRW 295  
RESULT 3  
ABBS0296  
ID ABBS0296 standard; protein; 362 AA.  
XX  
XX AC ABBS0296;  
XX  
XX 08-FEB-2002 (first entry)  
XX  
XX HLA-Cw ovarian tumour marker protein, SEQ ID NO:82.  
XX  
XX Ovarian tumour marker gene; human; overexpression; upregulation;  
XX epithelial tumour; cancer; diagnosis; prognosis; disease monitoring;  
XX identification; serous cystadenoma; borderline serous tumour;  
XX serous cystadenocarcinoma; mucinous cystadenocarcinoma;  
XX mucinous cystadenoma; borderline mucinous tumour; endometrioid carcinoma;  
XX undifferentiated carcinoma; clear cell adenocarcinoma; cystadenofibroma;  
XX adenofibroma; Brenner tumour; serial analysis of gene expression; SAGE;  
XX immune response pathway; cell proliferation regulation; protein folding;  
XX membrane localised; secreted; therapeutic target; cytostatic;  
XX gene therapy; vaccine.  
XX  
XX Homo sapiens.  
XX  
XX WO200175177-A2.  
XX  
XX 11-OCT-2001.  
XX  
XX 03-APR-2001; 2001WO-US010947.  
XX  
XX 03-APR-2000; 2000US-0194336P.  
XX  
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
XX  
XX Morin PJ, Sherman-Baust CA, Pizer ES, Hough CD;  
XX  
XX WPI; 2001-626450/72.  
XX N-PSDB; ABA83122.  
XX  
XX Detecting and identifying ovarian tumor, identifying increased risk for  
XX developing ovarian cancer, and determining effectiveness of ovarian  
XX cancer treatment, by measuring expression level of ovarian tumor marker  
XX gene.  
XX  
XX Claim 23; Page 126-127; 140pp; English.  
XX  
XX The invention relates to methods for diagnosing and prognosing ovarian  
XX tumours in an individual via the detection and measurement of the  
XX expression of ovarian tumour marker genes (ABA83081-ABA83122, ABA83180,  
XX ABA83182 and ABA83184) or segments thereof (ABA83123-ABA83169, ABA83179,  
XX ABA83181 and ABA83183). The methods of the invention are useful for  
XX assessing the relative severity of ovarian cancer, in prognostic tests for  
XX assessing the relative severity of ovarian cancer, in tests for  
XX monitoring a patient in remission from ovarian cancer and in tests for  
XX monitoring disease status in a patient being treated for ovarian cancer.  
XX The methods can additionally be used to identify a particular tumour as  
XX being an ovarian tumour (i.e., an epithelial ovarian tumour selected from  
XX serous cystadenoma, borderline serous tumour, serous cystadenocarcinoma,



KW allergic reaction; graft versus host disease; organ rejection;  
KW haemostatic; thrombolytic; cardiovascular disorder; infection;  
KW neurological disease; drug screening.

XX Homo sapiens.

XX WO20005350-A1.

XX 21-SEP-2000.

XX 08-MAR-2000; 2000WO-US005882.

XX 12-MAR-1999; 99US-0124270P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Rosen CA, Ruben SM;

XX WPI; 2000-587533/55.

XX N-PSDB; AAC78195.

XX Novel isolated nucleic acids comprising sequences encoding peptides  
XX useful for treating or diagnosing e.g. cancer.

XX Claim 11; Page 2115-2116; 2352pp; English.

XX AAC77607 to AAC78448 encode the human cancer associated proteins given in  
CC AAB43398 to AAB44239. The proteins can have activities based on the  
CC tissues and cells the genes are expressed in. Example of activities  
CC include: cytostatic; proliferative; vulnery; immunomodulator;  
CC antidiabetic; antiaesthetic; antirheumatic; antithrombotic;  
CC antiinflammatory; antithyroid; antiallergic; antibacterial; antiviral;  
CC dermatological; neuroprotective; cardiac; thrombolytic; coagulant;  
CC notropic; vasotropic; antipsoriatic and antiangiogenic. The  
CC polynucleotides and polypeptides can be used for preventing, treating or  
CC ameliorating medical conditions and diagnosing pathological conditions.  
CC Polynucleotides, polypeptides, antibodies, agonists and antagonists from  
CC the present invention may be used to treat immune disorders by activating  
CC or inhibiting the proliferation, differentiation or mobilisation of  
CC immune cells, to treat disorders of haematopoietic cells, autoimmune  
CC disorders, allergic reactions, graft versus host disease and organ  
CC rejection, modulate haemostatic or thrombolytic activity, modulate  
CC inflammation, cancers, cardiovascular disorders, neurological disease and  
CC bacterial or viral infections. The peptides, nucleotides, antibodies,  
CC agonists and antagonists may be also be used in drug screens. AAC78449 to  
CC AAC78457 and AAB44240 represent sequences used in the exemplification of  
CC the present invention

XX Sequence 271 AA;

Query Match 87.6%; Score 1311; DB 3; Length 271;  
Best Local Similarity 99.6%; Pred. No. 4.8e-116;  
Matches 241; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSHSLRYFSTAVSRPGGEPRIYAVEYVDDTQFLRFDSDAAIPRMEPREPWVQSGPQYW 60

DB 28 GSHSLRYFSTAVSRPGGEPRIYAVEYVDDTQFLRFDSDAAIPRMEPREPWVQSGPQYW 87

QY 61 EWTGTYAKANAQTDTRVALNLLRRYNQSEAGSHTLQGMNGCDMPDGRLLRGYHQAYDG 120

DB 88 EWTGTYAKANAQTDTRVALNLLRRYNQSEAGSHTLQGMNGCDMPDGRLLRGYHQAYDG 147

QY 121 KDYISLNEDLRSWTAADTVAQITQRFYAEAEYAEFPYILEGECLELLRRYLENGKETIQ 180

DB 148 KDYISLNEDLRSWTAADTVAQITQRFYAEAEYAEFPYILEGECLELLRRYLENGKETIQ 207

QY 181 RADPPKARVAHPHPSDHEATLRCAWLGYPAEITLTWQDGEQGTQDTELVEITRPAGDGT 240

DB 208 RADPPKARVAHPHPSDHEATLRCAWLGYPAEITLTWQDGEQGTQDTELVEITRPAGDGT 267

QY 241 FQ 242

DB 268 PR 269

RESULT 6

AAP80911

ID AAP80911 standard; protein; 274 AA.

XX AAP80911;

AC AAP80911;

XX 25-MAR-2003 (revised)

DT 18-SEP-1990 (first entry)

XX Consensus sequence of peptides which constitute the alpha-1, alpha-2 and

DE alpha-3 regions of a class I HLA molecule.

XX HLA-A2 epitopes; extracellular domains alpha-1, alpha-2 and alpha-3.

KW Homo sapiens.

XX Homo sapiens.

XX Key

FT Region

FT Region

FT Region

FT Region

FT Region

XX Location/Qualifiers

1..90

/note= "alpha-1 region"

91..180

/note= "alpha-2 region"

181..272

/note= "alpha-3 region"

XX WO8805784-A.

PN 11-AUG-1988.

XX 27-JAN-1988; 88WO-US000245.

PR 30-JAN-1987; 87US-00008846.

PR 24-DEC-1987; 87US-00138547.

XX (STRD ) UNIV LELAND STANFORD JUNIOR.

XX Krensky AM, Parham P, Clayberger C;

XX WPI; 1988-235147/33.

XX New peptide corresp. to major histocompatibility antigen regions - used

PT for modulating cytotoxic T-lymphocyte activity in e.g. transplants or

PT auto-immune diseases.

XX Example 9; Fig 4; 60pp; English.

XX The consensus sequence is derived from a total of 23 HLA-A,B,C sequences.

CC The protein sequences in the three extracellular domains (alpha-1, alpha-

CC 2 and alpha-3) are shown. The example concerned the effect of peptides

CC from different HLA-A2 epitopes on cytotoxicity of target cells by CTL of

CC different specificities. (Updated on 25-MAR-2003 to correct PF field.)

CC (Updated on 25-MAR-2003 to correct PR field.) (Updated on 25-MAR-2003 to

CC correct PA field.)

XX Sequence 274 AA;

QY Query Match 83.4%; Score 1248; DB 1; Length 274;

DB Best Local Similarity 82.8%; Pred. No. 4.8e-110;

Matches 227; Conservative 17; Mismatches 30; Indels 0; Gaps 0;

QY 1 GSHSLRYFSTAVSRPGGEPRIYAVEYVDDTQFLRFDSDAAIPRMEPREPWVQSGPQYW 60

DB 1 GSHSMRYFYFSTVSRPGGEPRIYAVEYVDDTQFLRFDSDAAIPRMEPREPWVQSGPQYW 60

QY 61 EWTGTYAKANAQTDTRVALNLLRRYNQSEAGSHTLQGMNGCDMPDGRLLRGYHQAYDG 120

DB 61 DRETQVKAQSTDRDLTLLRGYNQSEAGSHTLQGMNGCDMPDGRLLRGYHQAYDG 120

QY 121 KDYISLNEDLRSWTAADTVAQITQRFYAEAEYAEFPYILEGECLELLRRYLENGKETIQ 180

DB 121 KDYIALNEDLRSWTAADTVAQITQRFYAEAEYAEFPYILEGECLELLRRYLENGKETIQ 180

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QY 181 RADPPKAHVAHPISDHEATLRCWALGFYPAEITLTWQDGEEDQDTQDTVELVETRPAGDGT 240
DB 181 RADPPKTHVTHHPISDHEATLRCWALGFYPAEITLTWQDGEEDQDTQDTVELVETRPAGDGT 240
QY 241 FOKWAAVVVPSGEEQRYTCHVQHEGLPKPLTLRW 274
DB 241 FOKWAAVVVPSGEEQRYTCHVQHEGLPKPLTLRW 274

RESULT 7
AAP70155
ID AAP70155 standard; protein; 362 AA.
XX AC AAP70155;
XX DT 25-MAR-2003 (revised)
XX DT 10-MAR-1993 (revised)
XX DT 03-APR-1991 (first entry)
XX DE
XX DE HLA-B 27.
XX DE
XX KW Ankylosing spondylitis; rheumatic disorder; diagnosis.
XX OS Homo sapiens.
XX PN EP226069-A.
XX PD 24-JUN-1987.
XX PF 21-NOV-1986; 86EP-00116139.
XX PR 30-NOV-1985; 85DE-00542024.
XX PR 21-DEC-1985; 85DE-03545576.
XX PA (BEHW ) BEHRINGWERKE AG.
XX PI Szots H, Weiss E, Dörner C, Lang M, Meo T, Riethmülle G;
XX DR WPI; 1987-171469/25.
XX DR N-PSDB; AAN70225.
XX PT DNA coding for human histocompatibility antigen HLA-B 27 - useful for
XX PT diagnosis and antigen and antibody prodn.
XX PS Disclosure; Page 6; 13pp; German.
XX CC The DNA may be used to detect the HLA-B 27 gene (opt. mutated) in human
XX CC genetic material. The HLA-B 27 may be used to detect anti-HLA-B 27
XX CC antibodies in human serum. The antibodies may be used to determine HLA-B
XX CC 27 levels in human serum, eg for diagnosis of rheumatic disorders, esp.
XX CC ankylosing spondylitis. (Updated on 25-MAR-2003 to correct PR field.)
XX SQ Sequence 362 AA;
Query Match 82.1%; Score 1228; DB 1; Length 362;
Best Local Similarity 82.1%; Pred. No. 5 6e-108;
Matches 225; Conservative 14; Mismatches 35; Indels 0; Gaps 0;
QY 1 GSHSLRYFSTAVSRPGRGPRIYAVYDDTQFLRFDSDAAIPRMEPRPWEQGPQYW 60
DB 25 GSHSMRYFHTSVSRPGRGPRIYAVYDDTQFLRFDSDAAIPRMEPRPWEQGPQYW 84
QY 61 EWTTCYAKANAOTDRVALNLLRYNQSEAGSHTLQGMNGCDMPDGRLLRGYHQAIDG 120
DB 85 DRETQICKAKAQTDRDLTKLLRYNQSEAGSHTLQGMNGCDMPDGRLLRGYHQAIDG 144
QY 121 KQYISLNEDLSRSTAADTVAQITQRYEAEYAEFEPTYLEGECLELLRRYLENGKETLQ 180
DB 145 KQYIALNEDLSSTAADTVAQITQRYEAEYAEFEPTYLEGECLELLRRYLENGKETLQ 204
QY 181 RADPPKAHVAHPISDHEATLRCWALGFYPAEITLTWQDGEEDQDTQDTVELVETRPAGDGT 240
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DB 205 RADPPKTHVTHHPISDHEATLRCWALGFYPAEITLTWQDGEEDQDTQDTVELVETRPAGDRT 264
QY 241 FOKWAAVVVPSGEEQRYTCHVQHEGLPKPLTLRW 274
DB 265 FOKWAAVVVPSGEEQRYTCHVQHEGLPKPLTLRW 298

RESULT 8
AAP70590
ID AAP70590 standard; protein; 337 AA.
XX AC AAP70590;
XX DT 10-APR-1991 (first entry)
XX DE
XX DE Sequence of the human histocompatibility antigen HLA B27.
XX KW Rheumatic disorder; genetic screening; diagnosis; ankylosing spondylitis.
XX OS Homo sapiens.
XX PN DE3542024-A.
XX PD 04-JUN-1987.
XX PF 28-NOV-1985; 85DE-03542024.
XX PR 21-DEC-1985; 85DE-03545576.
XX PA (BEHW ) BEHRINGWERKE AG.
XX PI Riethmülle G, Meo T, Weiss E, Szots H;
XX DR WPI; 1987-157893/23.
XX DR N-PSDB; AAN70935.
XX PT DNA coding for antigen HLA B27 - and diagnostic reagents contg. such DNA,
XX PT antigen or antibody.
XX PS Disclosure; Page 5; 5pp; German.
XX CC The DNA may be used as a hybridisation probe for detecting the HLA B27
XX CC gene, eg for assessing susceptibility to rheumatic disorders such as
XX CC ankylosing spondylitis, or may be used to transform cells for prodn. of
XX CC HLA B27. The HLA B27 may be used to detect HLA B27 antibody in human
XX CC serum, or to produce mono- or polyclonal HLA B27 antibodies for use in
XX CC immunoassay
XX SQ Sequence 337 AA;
Query Match 82.1%; Score 1227.5; DB 1; Length 337;
Best Local Similarity 82.5%; Pred. No. 5.7e-108;
Matches 226; Conservative 14; Mismatches 33; Indels 1; Gaps 1;
QY 1 GSHSLRYFSTAVSRPGRGPRIYAVYDDTQFLRFDSDAAIPRMEPRPWEQGPQYW 60
DB 1 GSHSMRYFHTSVSRPGRGPRIYAVYDDTQFLRFDSDAAIPRMEPRPWEQGPQYW 60
QY 61 EWTTCYAKANAOTDRVALNLLRYNQSEAGSHTLQGMNGCDMPDGRLLRGYHQAIDG 120
DB 61 DRETQICKAKAQTDRDLTKLLRYNQSEAGSHTLQGMNGCDMPDGRLLRGYHQAIDG 119
QY 121 KQYISLNEDLSRSTAADTVAQITQRYEAEYAEFEPTYLEGECLELLRRYLENGKETLQ 180
DB 120 KQYIALNEDLSSTAADTVAQITQRYEAEYAEFEPTYLEGECLELLRRYLENGKETLQ 179
QY 181 RADPPKAHVAHPISDHEATLRCWALGFYPAEITLTWQDGEEDQDTQDTVELVETRPAGDGT 240
DB 180 RVDPPKTHVTHHPISDHEATLRCWALGFYPAEITLTWQDGEEDQDTQDTVELVETRPAGDRT 239
QY 241 FOKWAAVVVPSGEEQRYTCHVQHEGLPKPLTLRW 274
DB 240 FOKWAAVVVPSGEEQRYTCHVQHEGLPKPLTLRW 273
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RESULT 9  
 AAU32882  
 ID AAU32882 standard; protein; 369 AA.  
 XX  
 AC AAU32882;  
 XX  
 DT 18-DEC-2001 (first entry)  
 XX  
 DE Novel human secreted protein #3373.  
 XX  
 KW Human; vaccination; gene therapy; nutritional supplement;  
 KW stem cell proliferation; haematopoiesis; nerve tissue regeneration;  
 KW immune suppression; immune stimulation; anti-inflammatory; leukaemia.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200179449-A2.  
 XX  
 PD 25-OCT-2001.  
 XX  
 PF 16-APR-2001; 2001WO-US008656.  
 XX  
 PR 18-APR-2000; 2000US-00552929.  
 PR 26-JAN-2001; 2001US-00770160.  
 XX  
 PA (HYSE-) HYSEQ INC.  
 XX  
 PI Tang YT, Liu C, Drmanac RT;  
 XX  
 DR WPI; 2001-611725/70.  
 XX  
 PT Nucleic acids encoding a range of human polypeptides, useful in genetic  
 PT vaccination, testing and therapy.  
 XX  
 PS Claim 20; Page 683; 765pp; English.  
 XX  
 CC The invention relates to novel human secreted polypeptides. The  
 CC polypeptides and antibodies to the polypeptides are useful for  
 CC determining the presence of or predisposition to a disease associated  
 CC with altered levels of polypeptide. The polypeptides are also useful for  
 CC identifying agents (agonists and antagonists) that bind to them. Cells  
 CC expressing the proteins are useful for identifying a therapeutic agent  
 CC for use in treatment of a pathology related to aberrant expression or  
 CC physiological interactions of the polypeptide. Vectors comprising the  
 CC nucleic acids encoding the polypeptides and cells genetically engineered  
 CC to express them are also useful for producing the proteins. The proteins  
 CC are useful in genetic vaccination, testing and therapy, and can be used  
 CC as nutritional supplements. They may be used to increase stem cell  
 CC proliferation; to regulate haematopoiesis; and in bone, cartilage, tendon  
 CC and/or nerve tissue growth or regeneration; immune suppression and/or  
 CC stimulation; as anti-inflammatory agents; and in treatment of leukaemias.  
 CC AAU29510-AAU33304 represent the amino acid sequences of novel human  
 CC secreted proteins of the invention  
 XX  
 SQ Sequence 369 AA;  
 Query Match 81.8%; Score 1224; DB 4; Length 369;  
 Best Local Similarity 81.0%; Pred. No. 1.4e-107;  
 Matches 222; Conservative 21; Mismatches 31; Indels 0; Gaps 0;  
 QY 1 GSHSLRVPSTAVSRGGRGPRYIAVEYVDDTQFLRFDSDAAIPRMEPRFPWVEQGPQYW 60  
 DB 28 GSHSMRYFTDTSRPRGGRGPRFISVGYVDDTQFLRFDSDAASPRFPWVEQGPQYW 87  
 QY 61 EWTGYAKANAQTDRLVALNRLRRYQSEAGSHTLQGMGCDMGDPDGLRLRGVHQHAYDG 120  
 DB 88 DRNTQIFKNTQTDRSLRNRLRGYNQSEAGSHTLQSMYGDVDPDGLRLRGVHQHAYDG 147  
 QY 121 KDYISLNEDLSRWTAAADTAQITQRFYAEYAEFEFTYLEGECLELLRRYLENGKETLQ 180  
 DB 148 KDYIALNEDLSRWTAAADTAQITQRFYAEYAEFEFTYLEGECLELLRRYLENGKETLQ 207

QY 181 RADPPKAHVAHPISDHEATLRCWALGFYPAEITLTWQRDEGEQOTDELVELTRPAGDGT 240  
 DB 208 RADPPKTHVTHHPISDHEATLRCWALGFYPAEITLTWQRDEGEQOTDELVELTRPAGDRT 267  
 QY 241 FOKWAAVVVPSGEGEQRVTCHVQHEGLPQPLILRW 274  
 DB 268 FOKWAAVVVPSGEGEQRVTCHVQHEGLPQPLILRW 301  
 RESULT 10  
 AAU12465  
 ID AAU12465 standard; protein; 366 AA.  
 XX  
 AC AAU12465;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 29-AUG-1991 (first entry)  
 XX  
 DE HLA-C exon Cb-1.  
 XX  
 KW Human leukocyte antigen; probe; major histocompatibility complex; MHC;  
 KW class I.  
 XX  
 OS Homo sapiens.  
 XX  
 PN JP03112485-A.  
 XX  
 PD 14-MAY-1991.  
 XX  
 PF 22-SEP-1989; 89JP-00247695.  
 XX  
 PR 22-SEP-1989; 89JP-00247695.  
 XX  
 PA (OLYU ) OLYMPUS OPTICAL CO LTD.  
 XX  
 DR WPI; 1991-182989/25.  
 DR N-PSDB; AAQ12116.  
 XX  
 CC HLA-C gene, DNA probe and transformant cells - for immunisation of  
 CC animals and monoclonal antibody development.  
 XX  
 PS Claim 3; Page 2; 13pp; Japanese.  
 XX  
 CC Probes comprising part of the DNA sequence encoding the protein can be  
 CC used to identify Class I genes. The DNA can be expressed for immunisation  
 CC of animals and prodn. of monoclonal antibodies specific for the HLA-C  
 CC antigen. See also AAU12466 (same patent) and J03112486 and J03112487.  
 CC (Updated on 25-MAR-2003 to correct PA field.)  
 XX  
 SQ Sequence 366 AA;  
 Query Match 80.8%; Score 1209; DB 2; Length 366;  
 Best Local Similarity 81.7%; Pred. No. 3.7e-106;  
 Matches 223; Conservative 18; Mismatches 32; Indels 0; Gaps 0;  
 QY 2 SHSLRYFSTAVSRGGRGPRYIAVEYVDDTQFLRFDSDAAIPRMEPRFPWVEQGPQYWE 61  
 DB 26 SHSMRYFSTSVSRGGRGPRFIAVGVDVTQVRFSDAASPRFPWVEQGPQYWD 85  
 QY 62 WTTGYAKANAQTDRLVALNRLRRYQSEAGSHTLQGMGCDMGDPDGLRLRGVHQHAYDGK 121  
 DB 86 RETQKYRCAQTDRLVSLNRLRGYNQSEAGSHTLQWFGCDLGPDGLRLRGVHQHAYDGK 145  
 QY 122 DYISLNEDLSRWTAAADTAQITQRFYAEYAEFEFTYLEGECLELLRRYLENGKETLQ 181  
 DB 146 DYIALNEDLSRWTAAADTAQITQRFYAEYAEFEFTYLEGECLELLRRYLENGKETLQ 205  
 QY 182 ADPPKAHVAHPISDHEATLRCWALGFYPAEITLTWQRDEGEQOTDELVELTRPAGDGT 241  
 DB 206 AEPKTHVTHHPISDHEATLRCWALGFYPAEITLTWQRDEGEQOTDELVELTRPAGDGT 265  
 QY 242 QKWAADVVPSEGEQRVTCHVQHEGLPQPLILRW 274



QY 2 SHSLRYFSTAVSRGGEPRYIAVEYVDDTQFLRFSDAAIPRMEPRPWEQEGPYWE 61  
Db 34 SHSMRYFYTTAVSRGGEPRFIAGVYVDDTQFVRFSDDAASPRGEPAPWVEQEGPEYWD 93  
QY 62 WTTGYAKANAQTRVALNRLRRYNOSEAGSHTLQMGCDMGDPDGRLLRGYHQAIDCK 121  
Db 94 RETQYKROQTRVSLNRLRGYNOSEAGSHTLQMGCDLPGDGRLLRGYDQSAIDCK 153  
QY 122 DYISLNEDLSWTAADTVAQITQFYEAEBYAEFRYLEGECELELLRRYLENGKETLQ 181  
Db 154 DYIALNEHLASCTAADAQITQKWEAARAABQWRAYLEGTCVWLRRYLENGKETLQ 213  
QY 182 ADPPKAHVAHPISDHEATLRCWALGFYPAEITLTWQDGEBOFOTELVETRPAGDGT 241  
Db 214 AEPKKTHTVTHPVSDEATLRCWALGFYPAEITLTWQDGEDQDTQDELVETRPAGDGT 273  
QY 242 QKWAUVVPSGGEQRYTCHVQHEGLPOPLIRW 274  
Db 274 QKWAUVVPSGGEQRYTCHVQHEGLPEPLIRW 306

RESULT 13  
AAO06772  
ID AAO06772 standard; protein; 374 AA.

AC AAO06772;  
XX 06-NOV-2001 (first entry)  
XX Human polypeptide SEQ ID NO 20664.  
XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;  
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;  
KW tissue growth factor; immunomodulatory; cancer; leukaemia;  
KW nervous system disorders; arthritis; inflammation.  
XX Homo sapiens.  
XX WO200164835-A2.  
XX 07-SEP-2001.  
XX 26-FEB-2001; 2001WO-US004927.  
XX 28-FEB-2000; 2000US-00515126.  
XX 18-MAY-2000; 2000US-00577409.  
XX (HYSE-) HYSEQ INC.  
XX Tang YT, Liu C, Drmanac RT;  
XX WPI; 2001-514838/56.  
XX N-PSDB; AAI86703.

Isolated nucleic acids and polypeptides, useful for preventing diagnosing  
and treating e.g. leukemia, inflammation and immune disorders.  
XX  
PS Claim 20; SEQ ID NO 20664; 1399pp + Sequence Listing; English.

XX The invention relates to human polynucleotides (AAI79941-AAI93941) and  
CC the encoded proteins (AAO0010-AAO13910) that exhibit activity elating to  
CC cytokine, cell proliferation or cell differentiation or which may induce  
CC production of other cytokines in other cell populations. The  
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or  
CC peptide therapy. The polypeptides have various cytokine-like activities,  
CC e.g. stem cell growth factor activity, haematopoiesis regulating  
CC activity, tissue growth factor activity, immunomodulatory activity and  
CC activin/inhibin activity and may be useful in the diagnosis and/or  
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and  
CC inflammation. Note: The sequence data for this patent did not form part  
CC of the printed specification, but was obtained in electronic format  
CC directly from WIPO at [ftp.wipo.int/pub/published\\_pct\\_sequences](http://ftp.wipo.int/pub/published_pct_sequences)

SQ Sequence 374 AA;  
Query Match 80.5%; Score 1204.5; DB 4; Length 374;  
Best Local Similarity 81.8%; Pred. No. 1e-105;  
Matches 225; Conservative 15; Mismatches 34; Indels 1; Gaps 1;  
QY 1 GSHSLRYFSTAVSRGGEPRYIAVEYVDDTQFLRFSDAAIPRMEPRPWEQEGPYW 60  
Db 25 GSHSMRYFYTTAVSRGGEPRFIAGVYVDDTQFVRFSDDAASPRGEPAPWVEQEGPEY 84  
QY 61 EWTTCYAKANAQTRVALNRLRRYNOSEAGSHTLQMGCDMGDPDGRLLRGYHQAIDCG 120  
Db 85 DRETRNMKASQTYRENLRIRALRYNOSEAGSHTLQRMYGCDVPGDGRLLRGYHQAIDCG 144  
QY 121 KYISLNEDLSWTAADTVAQITQFYEAEBYAEFRYLEGECELELLRRYLENGKETLQ 180  
Db 145 KYIALNEHLASCTAADAQITQKWEAARAABQWRAYLEGTCVWLRRYLENGKETLQ 204  
QY 181 RADPPKAHVAHPISDHEATLRCWALGFYPAEITLTWQDGEBOFOTELVETRPAGDGT 240  
Db 205 RADPPKKTHTVTHPVSDEATLRCWALGFYPAEITLTWQDGEDQDTQDELVETRPAGDGT 264  
QY 241 FOKWAUVVPSGGEQRYTCHVQHEGLPOPLI-LRW 274  
Db 265 FOKWAUVVPSGGEQRYTCHVQHEGLPKPLTPERW 299

RESULT 14  
AAR03142  
ID AAR03142 standard; protein; 362 AA.

XX AAR03142;  
XX 25-MAR-2003 (revised)  
DT 19-MAR-1991 (first entry)  
XX Sequence of HLA-Bw52 antigen.  
XX DE  
XX KW Probe; HLA class I DNA; immunogen.  
XX OS Homo sapiens.  
XX PN BP354580-A.  
XX 14-FEB-1990.  
XX 10-AUG-1989; 89EP-00114857.  
XX 11-AUG-1988; 88JP-00200758.  
XX (OLYU ) OLYMPUS OPTICAL CO LTD.  
XX Kano K, Takiguchi M;  
XX WPI; 1990-046289/07.  
XX New DNA for class 1 human leucocyte antigens - with derived probes and  
XX transformed cells, used for DNA typing, as immunogens etc.  
XX Disclosure; Page 13; 23pp; English.

XX The HLA class I DNA can be used as a source of probes for use in DNA typing.  
CC transformed cells, which are useful as immunogens, can be obtained by  
CC introducing these DNAs into eucaryotic cells. (Updated on 25-MAR-2003 to  
CC correct PI field.)  
XX  
SQ Sequence 362 AA;

Query Match 80.3%; Score 1201; DB 2; Length 362;  
Best Local Similarity 80.3%; Pred. No. 2.1e-105;  
Matches 220; Conservative 20; Mismatches 34; Indels 0; Gaps 0;

QY 1 GSHSLRYFSTAVSRGGEPRYIAVEYVDDTQFLRFSDAAIPRMEPRPWEQEGPYW 60



Db 25 GSHSMRYFTAMSRPGRGEPFIAVGYVDDTQVRFDSDAASPRTEPRAPWIEQGEPEY 84  
QY 61 EWTGYAKANAQTRVALNLRNRYNQSEAGSHTLQGMNGCDMPDGRLLRGYHQHAYDG 120  
Db 85 DRETQSKNTQTYRENLRALRYNQSEAGSHTWQTMYGCDVGPDRLLRGHNQVAYDG 144  
QY 121 KDVISLNEDLRSTAAADTVAQITQRFYEAEVEEFTYLEGECLELLRYLNGKETLQ 180  
Db 145 KDYIALNEDLSSTAAADTAAQITQKWEAREAEQURAYLEGLCVBWRHRYLNGKETLQ 204  
QY 181 RADPPKAHVHPISDHEATLRCAWALGFYPAEITLTWQDGEQTDTELVEPTRPAGDGT 240  
Db 205 RADPPKTHVTHPVSDEATLRCAWALGFYPAEITLTWQDGEQTDTELVEPTRPAGDRT 264  
QY 241 FQKWAADVVPSEGEORYTCHVQHEGLPQPLILRW 274  
Db 265 FQKWAADVVPSEGEORYTCHVQHEGLPKPLILRW 298

RESULT 15

AD864171  
ID ADE64171 standard; protein; 362 AA.

XX ADE64171;

XX 29-JAN-2004 (first entry)

XX Human Protein P30474, SEQ ID NO 10123.

XX Human; pain; neuronal tissue; gene therapy;

KW spinal segmental nerve injury; chronic constriction injury; CCI;

KW spared nerve injury; SNI; Chung.

XX Homo sapiens.

XX W02003016475-A2.

XX 27-FEB-2003.

XX 14-AUG-2002; 2002WO-US025765.

XX 14-AUG-2001; 2001US-0312147P.

PR 01-NOV-2001; 2001US-0346382P.

PR 26-NOV-2001; 2001US-0333347P.

XX (GHEO ) GEN HOSPITAL CORP.

PA (FARB ) BAYER AG.

XX Woolf C, D'urso D, Befort K, Costigan M;

XX WPI; 2003-268312/26.

DR GENBANK; P30474.

XX New composition comprising two or more isolated polypeptides, useful for

PT preparing a medicament for treating pain in an animal.

XX Claim 1; Page; 1017pp; English.

XX The invention discloses a composition comprising two or more isolated rat  
XX or human polynucleotides or a polynucleotide which represents a fragment,  
XX derivative or allelic variation of the nucleic acid sequence. Also  
XX claimed are a vector comprising the novel polynucleotide, a host cell  
XX comprising the vector, a method for identifying a nucleotide sequence  
XX which is differentially regulated in an animal subjected to pain and a  
XX kit to perform the method, an array, a method for identifying an agent  
XX that increases or decreases the expression of the polynucleotide sequence  
XX that is differentially expressed in neuronal tissue of a first animal  
XX subjected to pain, a method for identifying a compound which regulates  
XX the expression of a polynucleotide sequence which is differentially  
XX expressed in an animal subjected to pain, a method for identifying a  
XX compound that regulates the activity of one or more of the  
XX polynucleotides, a method for producing a pharmaceutical composition, a

CC method for identifying a compound or small molecule that regulates the  
CC activity in an animal of one or more of the polypeptides given in the  
CC specification, a method for identifying a compound useful in treating  
CC pain and a pharmaceutical composition comprising the one or more  
CC polypeptides or their antibodies. The polynucleotide or the compound that  
CC modulates its activity is useful for preparing a medicament for treating  
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction  
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene  
CC therapy). The sequence presented is a human protein (shown in Table 2 of  
CC the specification) which is differentially expressed during pain. Note:  
CC The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic form directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences.

XX Sequence 362 AA;

Query Match 80.2%; Score 1200; DB 7; Length 362;

Best Local Similarity 80.3%; Pred. No. 2.6e-105;

Matches 220; Conservative 18; Mismatches 36; Indels 0; Gaps 0;

QY 1 GSHSLRYESTAVSRPGRGEPYIAVEYVDDTQFLRFSDAAIPRMEPREPWVEQGPQY 60

Db 25 GSHSMRYFTAMSRPGRGEPFIAVGYVDDTQVRFDSDAASPRTEPRAPWIEQGEPEY 84

QY 61 EWTGYAKANAQTRVALNLRNRYNQSEAGSHTLQGMNGCDMPDGRLLRGYHQHAYDG 120

Db 85 DRETQSKNTQTYRENLRALRYNQSEAGSHTWQTMYGCDVGPDRLLRGHNQVAYDG 144

QY 121 KDVISLNEDLRSTAAADTVAQITQRFYEAEVEEFTYLEGECLELLRYLNGKETLQ 180

Db 145 KDYIALNEDLSSTAAADTAAQITQKWEAREAEQURAYLEGLCVBWRHRYLNGKETLQ 204

QY 181 RADPPKAHVHPISDHEATLRCAWALGFYPAEITLTWQDGEQTDTELVEPTRPAGDGT 240

Db 205 RADPPKTHVTHPVSDEATLRCAWALGFYPAEITLTWQDGEQTDTELVEPTRPAGDRT 264

QY 241 FQKWAADVVPSEGEORYTCHVQHEGLPQPLILRW 274

Db 265 FQKWAADVVPSEGEORYTCHVQHEGLPKPLILRW 298

Search completed: June 18, 2004, 19:21:12

Job time : 63 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 18, 2004, 19:28:42 ; Search time 22 Seconds  
(without alignments)  
642.978 Million cell updates/sec

Title: US-09-819-371-5  
Perfect score: 274  
Sequence: 1 GSHSLRYFTAVSRPGRGP.....QRYTCHVQHEGLPQLILRW 274

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 389414 seqs, 51625971 residues

Word size : 0

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents AA.\*  
1: /cgn2\_6/prodata/2/iaa/5A COMB.pep.\*  
2: /cgn2\_6/prodata/2/iaa/5B COMB.pep.\*  
3: /cgn2\_6/prodata/2/iaa/6A COMB.pep.\*  
4: /cgn2\_6/prodata/2/iaa/6B COMB.pep.\*  
5: /cgn2\_6/prodata/2/iaa/PCITUS COMB.pep.\*  
6: /cgn2\_6/prodata/2/iaa/backfile1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	44	16.1	274	1	US-08-222-851-1
2	39	14.2	117	2	US-08-406-057-9
3	39	14.2	117	3	US-08-958-316-9
4	39	14.2	117	2	US-08-406-057-8
5	39	14.2	145	3	US-08-358-316-8
6	30	10.9	289	2	US-08-484-905-79
7	30	10.9	289	3	US-08-481-985B-79
8	30	10.9	289	3	US-08-370-476-79
9	29	10.6	274	2	US-08-484-905-105
10	29	10.6	274	2	US-08-484-905-107
11	29	10.6	274	2	US-08-484-905-108
12	29	10.6	274	3	US-08-481-985B-105
13	29	10.6	274	3	US-08-481-985B-107
14	29	10.6	274	3	US-08-481-985B-108
15	29	10.6	274	3	US-08-370-476-105
16	29	10.6	274	3	US-08-370-476-107
17	29	10.6	274	3	US-08-370-476-108
18	29	10.6	341	3	US-08-890-719-38
19	29	10.6	365	2	US-08-484-905-97
20	29	10.6	365	2	US-08-484-905-98
21	29	10.6	365	2	US-08-484-905-99
22	29	10.6	365	2	US-08-484-905-100
23	29	10.6	365	2	US-08-484-905-101
24	29	10.6	365	3	US-08-481-985B-97
25	29	10.6	365	3	US-08-481-985B-98
26	29	10.6	365	3	US-08-481-985B-99
27	29	10.6	365	3	US-08-481-985B-100

28	29	10.6	365	3	US-08-481-985B-101	Sequence 101, Appl
29	29	10.6	365	3	US-08-652-265-23	Sequence 23, Appl
30	29	10.6	365	3	US-08-834-437A-23	Sequence 23, Appl
31	29	10.6	365	3	US-08-370-476-97	Sequence 97, Appl
32	29	10.6	365	3	US-08-370-476-98	Sequence 98, Appl
33	29	10.6	365	3	US-08-370-476-99	Sequence 99, Appl
34	29	10.6	365	3	US-08-370-476-100	Sequence 100, Appl
35	29	10.6	365	3	US-08-370-476-101	Sequence 101, Appl
36	29	10.6	365	3	US-09-503-444A-23	Sequence 23, Appl
37	27	9.9	184	2	US-08-484-905-83	Sequence 83, Appl
38	27	9.9	184	3	US-08-481-985B-83	Sequence 83, Appl
39	27	9.9	184	3	US-08-370-476-83	Sequence 83, Appl
40	25	9.1	108	2	US-08-484-905-82	Sequence 82, Appl
41	25	9.1	108	3	US-08-481-985B-82	Sequence 82, Appl
42	25	9.1	108	3	US-08-370-476-82	Sequence 82, Appl
43	25	9.1	290	2	US-08-484-905-80	Sequence 80, Appl
44	25	9.1	290	3	US-08-481-985B-80	Sequence 80, Appl
45	25	9.1	290	3	US-08-370-476-80	Sequence 80, Appl

ALIGNMENTS

RESULT 1  
US-08-222-851-1  
; Sequence 1, Application US/08222851  
; Patent No. 5723128  
; GENERAL INFORMATION:  
; APPLICANT: CLAYBERGER, CAROL A.  
; APPLICANT: KEENSKY, ALAN M.  
; APPLICANT: PARHAM, PETER  
; TITLE OF INVENTION: CYTOTOXIC T-CELL LYMPHOCYTE ("CTL")  
; TITLE OF INVENTION: ACTIVITY REGULATION BY CLASS I MHC PEPTIDES  
; NUMBER OF SEQUENCES: 43  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORRISON & FOERSTER  
; STREET: 2000 PENNSYLVANIA AVENUE, NW, STE 5500  
; CITY: WASHINGTON  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20006-1812  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/222.851  
; FILING DATE: 05-APR-1994  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MILLMAN, ROBERT A.  
; REGISTRATION NUMBER: 36,217  
; REFERENCE/DOCKET NUMBER: 28600-20200.22  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 887-1500  
; TELEFAX: (202) 494-0792  
; TELEX: 90-4030 MRNFOERSWSH  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 274 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-222-851-1

Query Match 16.1%; Score 44; DB 1; Length 274;  
Best Local Similarity 100.0%; Pred.No. 1.2e-35;  
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 224 QTQDTVELVETPAGDGTQKWAIVVPSGEGQRYTCHVQHEGLP 267  
DB 224 QTQDTVELVETPAGDGTQKWAIVVPSGEGQRYTCHVQHEGLP 267

RESULT 2  
US-08-406-057-9  
; Sequence 9, Application US/08406057  
; Patent No. 5856442  
; GENERAL INFORMATION:  
; APPLICANT: CAROSELLA, EDGARDO D  
; APPLICANT: MOREAU, PHILIPPE  
; APPLICANT: GLUCKMAN, ELIANE  
; APPLICANT: KIRSZENBAUM, MAREK  
; TITLE OF INVENTION: TRANSCRIPTS OF THE MHC CLASS I HLA-G  
; TITLE OF INVENTION: GENE AND THEIR APPLICATIONS  
; NUMBER OF SEQUENCES: 15  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT  
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR  
; CITY: ARLINGTON  
; STATE: VIRGINIA  
; COUNTRY: USA  
; ZIP: 2202  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Tape  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/406,057  
; FILING DATE: 17-MAR-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: FR 94 03179  
; FILING DATE: 18-MAR-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: OBLON, NORMAN F  
; REGISTRATION NUMBER: 24,618  
; REFERENCE/DOCKET NUMBER: 846-331-0  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 413-3000  
; TELEFAX: (703) 413-2220  
; TELEX: 248855 OPAT UR  
; INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 117 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-406-057-9

Query Match 14.2%; Score 39; DB 2; Length 117;  
Best Local Similarity 100.0%; Pred. No. 4.8e-31;  
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 229 ELVETRPAGDGTFOKWAAVVPSGEEQRYTCHVQHEGLP 267  
|||||  
Db 51 ELVETRPAGDGTFOKWAAVVPSGEEQRYTCHVQHEGLP 89  
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RESULT 3  
US-08-958-316-9  
; Sequence 9, Application US/08958316  
; Patent No. 6291659  
; GENERAL INFORMATION:  
; APPLICANT: CAROSELLA, EDGARDO D  
; APPLICANT: MOREAU, PHILIPPE  
; APPLICANT: GLUCKMAN, ELIANE  
; APPLICANT: KIRSZENBAUM, MAREK  
; TITLE OF INVENTION: TRANSCRIPTS OF THE MHC CLASS I HLA-G  
; TITLE OF INVENTION: GENE AND THEIR APPLICATIONS  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT

; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR  
; CITY: ARLINGTON  
; STATE: VIRGINIA  
; COUNTRY: USA  
; ZIP: 2202  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Tape  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/958,316  
; FILING DATE: 27-OCT-1997  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: FR 94 03179  
; FILING DATE: 18-MAR-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: OBLON, NORMAN F  
; REGISTRATION NUMBER: 24,618  
; REFERENCE/DOCKET NUMBER: 0846-0437-0  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 413-3000  
; TELEFAX: (703) 413-2220  
; TELEX: 248855 OPAT UR  
; INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 117 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-958-316-9

Query Match 14.2%; Score 39; DB 3; Length 117;  
Best Local Similarity 100.0%; Pred. No. 4.8e-31;  
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 229 ELVETRPAGDGTFOKWAAVVPSGEEQRYTCHVQHEGLP 267  
|||||  
Db 51 ELVETRPAGDGTFOKWAAVVPSGEEQRYTCHVQHEGLP 89  
|||||

RESULT 4  
US-08-406-057-8  
; Sequence 8, Application US/08406057  
; Patent No. 5856442  
; GENERAL INFORMATION:  
; APPLICANT: CAROSELLA, EDGARDO D  
; APPLICANT: MOREAU, PHILIPPE  
; APPLICANT: GLUCKMAN, ELIANE  
; APPLICANT: KIRSZENBAUM, MAREK  
; TITLE OF INVENTION: TRANSCRIPTS OF THE MHC CLASS I HLA-G  
; TITLE OF INVENTION: GENE AND THEIR APPLICATIONS  
; NUMBER OF SEQUENCES: 15  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT  
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR  
; CITY: ARLINGTON  
; STATE: VIRGINIA  
; COUNTRY: USA  
; ZIP: 2202  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Tape  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/406,057  
; FILING DATE: 17-MAR-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: FR 94 03179

;; FILING DATE: 18-MAR-1994  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: OBLON, NORMAN F  
;; REGISTRATION NUMBER: 24,618  
;; REFERENCE/DOCKET NUMBER: 846-331-0  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (703) 413-3000  
;; TELEFAX: (703) 413-2220  
;; TELEX: 248855 OPAT UR  
;; INFORMATION FOR SEQ ID NO: 8:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 145 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
US-08-406-057-8

Query Match 14.2%; Score 39; DB 2; Length 145;  
Best Local Similarity 100.0%; Pred. No. 5.9e-31;  
Matches 39; Conservative 0; Mismatches 0; Indels 0;

QY 229 ELVETRPAGDGTFOKWAAVVPSGEEQRYTCHVQHEGLP 267  
Db 79 ELVETRPAGDGTFOKWAAVVPSGEEQRYTCHVQHEGLP 117

RESULT 5  
US-08-958-316-8  
; Sequence 8, Application US/08958316  
; Patent No. 6291659  
; GENERAL INFORMATION:  
; APPLICANT: CAROSELLA, EDGARDO D  
; APPLICANT: MOREAU, PHILIPPE  
; APPLICANT: GLUCKMAN, ELIANE  
; APPLICANT: KIRSZENBAUM, MAREK  
; TITLE OF INVENTION: TRANSCRIPTS OF THE MHC CLASS I HLA-G  
; TITLE OF INVENTION: GENE AND THEIR APPLICATIONS  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT  
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR  
; CITY: ARLINGTON  
; STATE: VIRGINIA  
; COUNTRY: USA  
; ZIP: 2202  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Tape  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION NUMBER: US/08/958,316  
; FILING DATE: 27-OCT-1997  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: FR 94 03179  
; FILING DATE: 18-MAR-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: OBLON, NORMAN F  
; REGISTRATION NUMBER: 24,618  
; REFERENCE/DOCKET NUMBER: 0846-0437-0  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 413-3000  
; TELEFAX: (703) 413-2220  
; TELEX: 248855 OPAT UR  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 145 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide

US-08-958-316-8

Query Match 14.2%; Score 39; DB 3; Length 145;  
Best Local Similarity 100.0%; Pred. No. 5.9e-31;  
Matches 39; Conservative 0; Mismatches 0; Indels 0;

QY 229 ELVETRPAGDGTFOKWAAVVPSGEEQRYTCHVQHEGLP 267  
Db 79 ELVETRPAGDGTFOKWAAVVPSGEEQRYTCHVQHEGLP 117

RESULT 6  
US-08-484-905-79  
; Sequence 79, Application US/08484905  
; Patent No. 5976551  
; GENERAL INFORMATION:  
; APPLICANT: Mottez, Estelle  
; APPLICANT: Abastado, Jean-Pierre  
; APPLICANT: Kourilsky, Philippe  
; TITLE OF INVENTION: An Altered Major Histocompatibility  
; TITLE OF INVENTION: Complex (MHC) Determinant and Methods for Using the  
; TITLE OF INVENTION: Determinant  
; NUMBER OF SEQUENCES: 127  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &  
; STREET: 1300 I Street, N.W., Suite 700  
; CITY: Washington  
; STATE: D.C.  
; ZIP: 20005-3315  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy Disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/484,905  
; FILING DATE: 07-JUNE-1995  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/801,818  
; FILING DATE: 05-DEC-1991  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/792,473  
; FILING DATE: 15-NOV-1991  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Potter, Jane E. R.  
; REGISTRATION NUMBER: 33,332  
; REFERENCE/DOCKET NUMBER: 03495.0106-03000  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-408-4000  
; TELEFAX: 202-408-4400  
; INFORMATION FOR SEQ ID NO: 79:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 289 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-484-905-79

Query Match 10.9%; Score 30; DB 2; Length 289;  
Best Local Similarity 100.0%; Pred. No. 9.4e-22;  
Matches 30; Conservative 0; Mismatches 0; Indels 0;

QY 226 QDELVETRPAGDGTFOKWAAVVPSGEEQ 255  
Db 226 QDELVETRPAGDGTFOKWAAVVPSGEEQ 255

RESULT 7  
US-08-481-985B-79

; Sequence 79, Application US/08481985B  
; Patent No. 6011146  
; GENERAL INFORMATION:  
; APPLICANT: Mottez, Estelle  
; APPLICANT: Abastado, Jean-Pierre  
; APPLICANT: Kourilsky, Philippe  
; TITLE OF INVENTION: Altered Major Histocompatibility Complex  
; NUMBER OF SEQUENCES: 148  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &  
; ADDRESSEE: Dunner  
; STREET: 1300 I Street, N.W., Suite 700  
; CITY: Washington  
; STATE: D.C.  
; ZIP: 20005-3315  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/481,985B  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/801,818  
; FILING DATE: 05-DEC-1991  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/792,473  
; FILING DATE: 15-NOV-1991  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Meyers, Kenneth J.  
; REGISTRATION NUMBER: 25,146  
; REFERENCE/DOCKET NUMBER: 03495.0106-04000  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-408-4000  
; TELEFAX: 202-408-4400  
; INFORMATION FOR SEQ ID NO: 79:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 289 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-481-985B-79

Query Match 10.9%; Score 30; DB 3; Length 289;  
Best Local Similarity 100.0%; Pred. No. 9.4e-22;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 226 QDTLVETRPAGDGTFOKWAAVVPSGEQ 255  
Db 226 QDTLVETRPAGDGTFOKWAAVVPSGEQ 255

RESULT 8  
US-08-370-476-79  
; Sequence 79, Application US/08370476  
; Patent No. 6153408  
; GENERAL INFORMATION:  
; APPLICANT: Mottez, Estelle  
; APPLICANT: Abastado, Jean-Pierre  
; APPLICANT: Kourilsky, Philippe  
; APPLICANT: Lone, Yu-Chun  
; APPLICANT: Ojcius, David  
; APPLICANT: Casrouge, Armanda  
; TITLE OF INVENTION: Altered Major Histocompatibility Complex  
; NUMBER OF SEQUENCES: 127  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &

; ADDRESSEE: Dunner  
; STREET: 1300 I Street, N.W., Suite 700  
; CITY: Washington  
; STATE: D.C.  
; ZIP: 20005-3315  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/370,476  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/117,575  
; FILING DATE: 07-SEP-1993  
; APPLICATION NUMBER: US 08/072,787  
; FILING DATE: 06-JUN-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/801,818  
; FILING DATE: 05-DEC-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/792,473  
; FILING DATE: 15-NOV-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Meyers, Kenneth J.  
; REGISTRATION NUMBER: 25,146  
; REFERENCE/DOCKET NUMBER: 05243.0001-01000  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-408-4000  
; TELEFAX: 202-408-4400  
; INFORMATION FOR SEQ ID NO: 79:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 289 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-370-476-79

Query Match 10.9%; Score 30; DB 3; Length 289;  
Best Local Similarity 100.0%; Pred. No. 9.4e-22;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 226 QDTLVETRPAGDGTFOKWAAVVPSGEQ 255  
Db 226 QDTLVETRPAGDGTFOKWAAVVPSGEQ 255

RESULT 9  
US-08-484-905-105  
; Sequence 105, Application US/08484905  
; Patent No. 5976551  
; GENERAL INFORMATION:  
; APPLICANT: Mottez, Estelle  
; APPLICANT: Abastado, Jean-Pierre  
; APPLICANT: Kourilsky, Philippe  
; TITLE OF INVENTION: An Altered Major Histocompatibility  
; TITLE OF INVENTION: Complex(MHC) Determinant and Methods for Using the  
; TITLE OF INVENTION: Determinant  
; NUMBER OF SEQUENCES: 127  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &  
; ADDRESSEE: Dunner  
; STREET: 1300 I Street, N.W., Suite 700  
; CITY: Washington  
; STATE: D.C.  
; ZIP: 20005-3315  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy Disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS-/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,905
; FILING DATE: 07-JUNE-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/801,818
; FILING DATE: 05-DEC-1991
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/792,473
; FILING DATE: 15-NOV-1991
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Potter, Jane E. R.
; REGISTRATION NUMBER: 33,332
; REFERENCE/DOCKET NUMBER: 03495.0106-03000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4400
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 105:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 274 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-484-905-105

Query Match 10.6%; Score 29; DB 2; Length 274;
Best Local Similarity 100.0%; Pred. No. 8.8e-21;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 224 QTQDTLVELTRPAGDGTQKWAAVVPSG 252
Db 224 QTQDTLVELTRPAGDGTQKWAAVVPSG 252

RESULT 11
US-08-484-905-108
; Sequence 108, Application US/08484905
; Patent No. 5976551
; GENERAL INFORMATION:
; APPLICANT: Mottez, Estelle
; APPLICANT: Abastado, Jean-Pierre
; APPLICANT: Kourilsky, Philippe
; TITLE OF INVENTION: An Altered Major Histocompatibility
; TITLE OF INVENTION: Complex(MHC) Determinant and Methods for Using the
; NUMBER OF SEQUENCES: 127
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W., Suite 700
; CITY: Washington
; STATE: D.C.
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS-/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,905
; FILING DATE: 07-JUNE-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/801,818
; FILING DATE: 05-DEC-1991
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/792,473
; FILING DATE: 15-NOV-1991
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Potter, Jane E. R.
; REGISTRATION NUMBER: 33,332
; REFERENCE/DOCKET NUMBER: 03495.0106-03000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4400
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 108:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 274 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-484-905-108

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Query Match      10.6%; Score 29; DB 2; Length 274;
Best Local Similarity 100.0%; Pred. No. 8.8e-21;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 224 QTQDTLVETRPAGDGTGFKWAAVVVPSG 252
Db 224 QTQDTLVETRPAGDGTGFKWAAVVVPSG 252

RESULT 12
US-08-481-985B-105
; Sequence 105, Application US/08481985B
; Patent No. 6011146
; GENERAL INFORMATION:
; APPLICANT: Mottez, Estelle
; APPLICANT: Abastado, Jean-Pierre
; APPLICANT: Kourilsky, Philippe
; TITLE OF INVENTION: Altered Major Histocompatibility Complex
; TITLE OF INVENTION:
; NUMBER OF SEQUENCES: 148
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W., Suite 700
; CITY: Washington
; STATE: D.C.
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/481,985B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/801,818
; FILING DATE: 05-DEC-1991
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/792,473
; FILING DATE: 15-NOV-1991
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 03495.0106-04000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 105:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 274 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-481-985B-107

Query Match      10.6%; Score 29; DB 3; Length 274;
Best Local Similarity 100.0%; Pred. No. 8.8e-21;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 224 QTQDTLVETRPAGDGTGFKWAAVVVPSG 252
Db 224 QTQDTLVETRPAGDGTGFKWAAVVVPSG 252

RESULT 14
US-08-481-985B-108
; Sequence 108, Application US/08481985B
; Patent No. 6011146
; GENERAL INFORMATION:
; APPLICANT: Mottez, Estelle
; APPLICANT: Abastado, Jean-Pierre
; APPLICANT: Kourilsky, Philippe
; TITLE OF INVENTION: Altered Major Histocompatibility Complex
; TITLE OF INVENTION:
; NUMBER OF SEQUENCES: 148
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W., Suite 700
; CITY: Washington
; STATE: D.C.
; ZIP: 20005-3315
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COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/481,985B  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/801,818  
FILING DATE: 05-DEC-1991  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/792,473  
FILING DATE: 15-NOV-1991  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Meyers, Kenneth J.  
REGISTRATION NUMBER: 25,146  
REFERENCE/DOCKET NUMBER: 03495.0106-04000  
TELEPHONE: 202-408-4400  
TELEFAX: 202-408-4400  
INFORMATION FOR SEQ ID NO: 108:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 274 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-481-985B-108

Query Match 10.6%; Score 29; DB 3; Length 274;  
Best Local Similarity 100.0%; Pred. No. 8.8e-21;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 224 QTQDTLVETRPAGDGTFOKWAAVVPSG 252  
DB 224 QTQDTLVETRPAGDGTFOKWAAVVPSG 252

RESULT 15  
US-08-370-476-105  
Sequence 105, Application US/08370476  
Patent No. 6153408  
GENERAL INFORMATION:  
APPLICANT: Mottez, Estelle  
APPLICANT: Abastado, Jean-Pierre  
APPLICANT: Kourilsky, Philippe  
APPLICANT: Lone, Yu-Chun  
APPLICANT: Ojcius, David  
APPLICANT: Carrouge, Armande  
TITLE OF INVENTION: Altered Major Histocompatibility Complex  
TITLE OF INVENTION: 127  
NUMBER OF SEQUENCES: 127  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &  
ADDRESSEE: Dunner  
STREET: 1300 I Street, N.W., Suite 700  
CITY: Washington  
STATE: D.C.  
ZIP: 20005-3315  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/370,476  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/117,575

FILING DATE: 07-SEP-1993  
APPLICATION NUMBER: US 08/072,787  
FILING DATE: 06-JUN-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/801,818  
FILING DATE: 05-DEC-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/792,473  
FILING DATE: 15-NOV-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Meyers, Kenneth J.  
REGISTRATION NUMBER: 25,146  
REFERENCE/DOCKET NUMBER: 05243.0001-01000  
TELEPHONE: 202-408-4400  
TELEFAX: 202-408-4400  
INFORMATION FOR SEQ ID NO: 105:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 274 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-370-476-105

Query Match 10.6%; Score 29; DB 3; Length 274;  
Best Local Similarity 100.0%; Pred. No. 8.8e-21;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 224 QTQDTLVETRPAGDGTFOKWAAVVPSG 252  
DB 224 QTQDTLVETRPAGDGTFOKWAAVVPSG 252

Search completed: June 18, 2004, 19:32:29  
Job time : 23 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 18, 2004, 19:25:36 ; Search time 22 Seconds  
(without alignments)  
642.978 Million cell updates/sec

Title: US-09-819-371-5  
Perfect score: 1496  
Sequence: 1 GSHSLRYFSTAVSRGGEPRP.....QRYTCHVQHGILPQPIILRW 274

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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3: /cgn2\_6/ptodata/2/iaa/6A COMB.pdp.\*  
4: /cgn2\_6/ptodata/2/iaa/6B COMB.pdp.\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1248	83.4	274	1	US-08-222-851-1
2	1154	77.1	365	2	US-08-484-905-100
3	1154	77.1	365	3	US-08-481-985B-100
4	1154	77.1	365	3	US-08-652-265-23
5	1154	77.1	365	3	US-08-834-497A-23
6	1154	77.1	365	3	US-08-370-476-100
7	1154	77.1	365	3	US-08-503-444A-23
8	1153	77.1	341	3	US-08-890-719-38
9	1151	76.9	365	2	US-08-484-905-99
10	1151	76.9	365	2	US-08-484-905-104
11	1151	76.9	365	3	US-08-481-985B-99
12	1151	76.9	365	3	US-08-481-985B-104
13	1151	76.9	365	3	US-08-370-476-99
14	1151	76.9	365	3	US-08-370-476-104
15	1150	76.9	274	2	US-08-484-905-107
16	1150	76.9	274	2	US-08-484-905-108
17	1150	76.9	274	3	US-08-481-985B-107
18	1150	76.9	274	3	US-08-481-985B-108
19	1150	76.9	274	3	US-08-370-476-107
20	1150	76.9	274	3	US-08-370-476-108
21	1147	76.7	365	2	US-08-484-905-97
22	1147	76.7	365	2	US-08-484-905-98
23	1147	76.7	365	3	US-08-481-985B-97
24	1147	76.7	365	3	US-08-481-985B-98
25	1147	76.7	365	3	US-08-370-476-97
26	1147	76.7	365	3	US-08-370-476-98
27	1146	76.6	274	2	US-08-484-905-105

28	1146	76.6	274	3	US-08-481-985B-105	Sequence 105, App
29	1146	76.6	274	3	US-08-370-476-105	Sequence 105, App
30	1142	76.3	274	2	US-08-484-905-106	Sequence 106, App
31	1142	76.3	274	3	US-08-481-985B-106	Sequence 106, App
32	1142	76.3	274	3	US-08-370-476-106	Sequence 106, App
33	1142	76.3	365	2	US-08-484-905-103	Sequence 103, App
34	1142	76.3	365	3	US-08-481-985B-103	Sequence 103, App
35	1142	76.3	365	3	US-08-370-476-103	Sequence 103, App
36	1141	76.3	365	2	US-08-484-905-102	Sequence 102, App
37	1141	76.3	365	3	US-08-481-985B-102	Sequence 102, App
38	1141	76.3	365	3	US-08-370-476-102	Sequence 101, App
39	1133	75.7	365	2	US-08-484-905-101	Sequence 101, App
40	1133	75.7	365	3	US-08-481-985B-101	Sequence 101, App
41	1133	75.7	365	3	US-08-370-476-101	Sequence 101, App
42	1097	73.3	361	3	US-08-652-265-22	Sequence 22, Appl
43	1097	73.3	361	3	US-08-834-497A-22	Sequence 22, Appl
44	1097	73.3	361	3	US-09-503-444A-22	Sequence 22, Appl
45	1071	71.6	361	4	US-08-914-372C-8	Sequence 8, Appl

ALIGNMENTS

RESULT 1  
US-08-222-851-1  
; Sequence 1, Application US/08222851  
; Patent No. 5723128  
; GENERAL INFORMATION:  
; APPLICANT: CLAYBERGER, CAROL A.  
; APPLICANT: KRENSKY, ALAN M.  
; APPLICANT: PARHAM, PETER  
; TITLE OF INVENTION: CYTOTOXIC T-CELL LYMPHOCYTE ("CTL")  
; TITLE OF INVENTION: ACTIVITY REGULATION BY CLASS I MHC PEPTIDES  
; NUMBER OF SEQUENCES: 43  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORRISON & FORSTER  
; STREET: 2000 PENNSYLVANIA AVENUE, NW, STE 5500  
; CITY: WASHINGTON  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20006-1812  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/222,851  
; FILING DATE: 05-APR-1994  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MILLMAN, ROBERT A.  
; REGISTRATION NUMBER: 36,217  
; REFERENCE/DOCKET NUMBER: 28600-20200.22  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 887-1500  
; TELEFAX: (202) 494-0792  
; TELEX: 90-4030 MRGNFORSHWSH  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 274 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear

Query Match 83.4%; Score 1248; DB 1; Length 274;  
Best Local Similarity 82.6%; Pred. No. 4.3e-114;  
Matches 227; Conservative 17; Mismatches 30; Indels 0; Gaps 0;

QY 1 GSHSLRYFSTAVSRGGEPRYIAVEYVDDTQFLRFDSDAAIPRMEPRFPWQEQPW 60  
DB 1 GSHSMRYFTYSVRGGEPRYIAVGYVDDTQFLRFDSDAASPRMEPRAPWIEQGEPEW 60

QY 61 EWTGYAKANAQTDVALRNLLRYNQSEAGSHTLQMGNCMDGPDGRLRLRYHQHAYDG 120  
DB 61 DRETOIKVAQSDTDREDLRTLRLGYNQSEAGSHTIQRMYGCDVGPDGRLLRGLYHQHAYDG 120  
QY 121 KDYISLNEDELRSWTAADTVAQITQRFYAEAEFEFTYLEGECLELLRRYLENGKETLQ 180  
DB 121 KDYIALNEDELRSWTAADTVAQITQRFYAEAEFEFTYLEGECLELLRRYLENGKETLQ 180  
QY 181 RADPPKARVAHPISDHEATLRCWALGFYPAEITLTWQDGEEOQDTQDTLTVETRPAGDGT 240  
DB 181 RADPPKTHVTHPISDHEATLRCWALGFYPAEITLTWQDGEEOQDTQDTLTVETRPAGDGT 240  
QY 241 FQKAAVVVPSEGEQRYTCHVQHEGLPQPLILRW 274  
DB 241 FQKAAVVVPSEGEQRYTCHVQHEGLPQPLILRW 274

RESULT 2  
US-08-484-905-100  
; Sequence 100, Application US/08484905  
; Patent No. 5976551  
; GENERAL INFORMATION:  
; APPLICANT: Mottez, Estelle  
; APPLICANT: Abastado, Jean-Pierre  
; APPLICANT: Kourilsky, Philippe  
; TITLE OF INVENTION: An Altered Major Histocompatibility  
; TITLE OF INVENTION: Complex(MHC) Determinant and Methods for Using the  
; TITLE OF INVENTION: Determinant  
; NUMBER OF SEQUENCES: 127  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &  
; ADDRESSEE: Dunner  
; STREET: 1300 I Street, N.W., Suite 700  
; CITY: Washington  
; STATE: D.C.  
; ZIP: 20005-3315  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/484,905  
; FILING DATE: 07-JUNE-1995  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/801,818  
; FILING DATE: 05-DEC-1991  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/792,473  
; FILING DATE: 15-NOV-1991  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Potter, Jane E. R.  
; REGISTRATION NUMBER: 33,332  
; REFERENCE/DOCKET NUMBER: 03495.0106-03000  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-408-4000  
; TELEFAX: 202-408-4400  
; INFORMATION FOR SEQ ID NO: 100:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 365 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-484-905-100

Query Match 77.1%; Score 1154; DB 2; Length 365;  
Best Local Similarity 76.6%; Pred. No. 1e-104;  
Matches 210; Conservative 22; Mismatches 42; Indels 0; Gaps 0;

QY 1 GSHSLRYSTAVSRGRGEPRIAYVEYVDDTQFLRFSDDAAIPRMEPREPWVEQBPQYW 60  
DB 25 GSHSMRYFYTSVSRGRGEPRIAYVYDDTQFLRFSDDAAIPRMEPREPWVEQBPQYW 84  
QY 61 EWTGYAKANAQTDVALRNLLRYNQSEAGSHTLQMGNCMDGPDGRLRLRYHQHAYDG 120  
DB 85 DGETRKVAHSAQTHRVLDLSTLRGYNQSEAGSHTVQRMFGCDVGSDFRLRGYHQHAYDG 144  
QY 121 KDYISLNEDELRSWTAADTVAQITQRFYAEAEFEFTYLEGECLELLRRYLENGKETLQ 180  
DB 145 KDYIALNEDELRSWTAADTVAQITQRFYAEAEFEFTYLEGECLELLRRYLENGKETLQ 204  
QY 181 RADPPKARVAHPISDHEATLRCWALGFYPAEITLTWQDGEEOQDTQDTLTVETRPAGDGT 240  
DB 205 RTDAPKTHVTHPISDHEATLRCWALGFYPAEITLTWQDGEEOQDTQDTLTVETRPAGDGT 264  
QY 241 FQKAAVVVPSEGEQRYTCHVQHEGLPQPLILRW 274  
DB 265 FQKAAVVVPSEGEQRYTCHVQHEGLPQPLILRW 298

RESULT 3  
US-08-481-985B-100  
; Sequence 100, Application US/08481985B  
; Patent No. 6011146  
; GENERAL INFORMATION:  
; APPLICANT: Mottez, Estelle  
; APPLICANT: Abastado, Jean-Pierre  
; APPLICANT: Kourilsky, Philippe  
; TITLE OF INVENTION: Altered Major Histocompatibility Complex  
; TITLE OF INVENTION:  
; NUMBER OF SEQUENCES: 148  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &  
; ADDRESSEE: Dunner  
; STREET: 1300 I Street, N.W., Suite 700  
; CITY: Washington  
; STATE: D.C.  
; ZIP: 20005-3315  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/481,985B  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/801,818  
; FILING DATE: 05-DEC-1991  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/792,473  
; FILING DATE: 15-NOV-1991  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Meyers, Kenneth J.  
; REGISTRATION NUMBER: 25,146  
; REFERENCE/DOCKET NUMBER: 03495.0106-04000  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-408-4000  
; TELEFAX: 202-408-4400  
; INFORMATION FOR SEQ ID NO: 100:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 365 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-481-985B-100

Query Match 77.1%; Score 1154; DB 3; Length 365;  
Best Local Similarity 76.6%; Pred. No. 1e-104;

Matches 210; Conservative 22; Mismatches 42; Indels 0; Gaps 0;

QY 1 GSHSLYFSTAVSRPGGEPRIYAVYVDDTQFLRDSDAAI PRMEPRPWWEGPOYW 60  
DB 25 GSHSMRYFTSVSRPGGEPRIYAVYVDDTQFLRDSDAAI PRMEPRPWWEGPOYW 84  
QY 61 EMTTGYAKANAQDRVALNLLRRYNOSEAGSHTLQGMNGCDMPDGRLLRGYHAYDG 120  
DB 85 DGETRKVAHQSOTHRVDLTLRGYNOSEAGSHTLQGMNGCDMPDGRLLRGYHAYDG 144  
QY 121 KYISLNEDLSRWTAAADTVAQITQFYEAEEYAEFPRTYLEGECLELLRRYLENGKETLQ 180  
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QY 181 RADPPKAHVAHPISDHEATLRCWALGFYPAEITLTWQDGEBOOTDTLVELTRPAGDGT 240  
DB 205 RTDAPKTHMTHAVSDHEATLRCWALGFYPAEITLTWQDGEBOOTDTLVELTRPAGDGT 264  
QY 241 FQKAAVVVPSGGEQRYTCHVQHEGLPQPLIRW 274  
DB 265 FQKAAVVVPSGGEQRYTCHVQHEGLPQPLIRW 298

RESULT 4  
US-08-652-265-23  
; Sequence 23, Application US/08652265  
; Patent No. 6025130  
; GENERAL INFORMATION:  
; APPLICANT: Thomas, Winston J.  
; APPLICANT: Drayna, Dennis T.  
; APPLICANT: Feder, John N.  
; APPLICANT: Gnirke, Andreas  
; APPLICANT: Ruddy, David  
; APPLICANT: Tsuchihashi, Zenta  
; APPLICANT: Wolff, Roger K.  
; TITLE OF INVENTION: Hereditary Hemochromatosis Gene  
; NUMBER OF SEQUENCES: 44  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA: US/08/652,265  
; APPLICATION NUMBER: US/08/652,265  
; FILING DATE: 23-MAY-1996  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Smith, William M.  
; REGISTRATION NUMBER: 30,223  
; REFERENCE/DOCKET NUMBER: 17957-000500  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 23:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 365 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; FEATURE:  
; NAME/KEY: Protein  
; LOCATION: 1..365  
; OTHER INFORMATION: /note= "Human Major Histocompatibility  
; CLASS I (MHC) protein"  
US-08-652-265-23

Query Match 77.1%; Score 1154; DB 3; Length 365;  
Best Local Similarity 77.0%; Pred. No. 1e-104;  
Matches 211; Conservative 21; Mismatches 42; Indels 0; Gaps 0;

QY 1 GSHSLYFSTAVSRPGGEPRIYAVYVDDTQFLRDSDAAI PRMEPRPWWEGPOYW 60  
DB 25 GSHSMRYFTSVSRPGGEPRIYAVYVDDTQFLRDSDAAI PRMEPRPWWEGPOYW 84  
QY 61 EMTTGYAKANAQDRVALNLLRRYNOSEAGSHTLQGMNGCDMPDGRLLRGYHAYDG 120  
DB 85 DGETRKVAHQSOTHRVDLTLRGYNOSEAGSHTLQGMNGCDMPDGRLLRGYHAYDG 144  
QY 121 KYISLNEDLSRWTAAADTVAQITQFYEAEEYAEFPRTYLEGECLELLRRYLENGKETLQ 180  
DB 145 KDYIALKEDLSRWTAAADTVAQITQFYEAEEYAEFPRTYLEGECLELLRRYLENGKETLQ 204  
QY 181 RADPPKAHVAHPISDHEATLRCWALGFYPAEITLTWQDGEBOOTDTLVELTRPAGDGT 240  
DB 205 RTDAPKTHMTHAVSDHEATLRCWALGFYPAEITLTWQDGEBOOTDTLVELTRPAGDGT 264  
QY 241 FQKAAVVVPSGGEQRYTCHVQHEGLPQPLIRW 274  
DB 265 FQKAAVVVPSGGEQRYTCHVQHEGLPQPLIRW 298

RESULT 5  
US-08-834-497A-23  
; Sequence 23, Application US/08834497A  
; Patent No. 6140305  
; GENERAL INFORMATION:  
; APPLICANT: Thomas, Winston J.  
; APPLICANT: Drayna, Dennis T.  
; APPLICANT: Feder, John N.  
; APPLICANT: Gnirke, Andreas  
; APPLICANT: Ruddy, David  
; APPLICANT: Tsuchihashi, Zenta  
; APPLICANT: Wolff, Roger K.  
; TITLE OF INVENTION: HEREDITARY HEMOCHROMATOSIS GENE PRODUCTS  
; NUMBER OF SEQUENCES: 76  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds LLP  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036-2811  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: Windows 95  
; SOFTWARE: FastSeq for Windows Version 2.0b  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/834,497A  
; FILING DATE: 04-APR-1997  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/652,265  
; FILING DATE: 23-MAY-1996  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/632,673  
; FILING DATE: 16-APR-1996  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/630,912  
; FILING DATE: 04-APR-1996  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Poissant, Brian M.  
; REGISTRATION NUMBER: 28,462  
; REFERENCE/DOCKET NUMBER: 8907-0056-999  
; TELECOMMUNICATION INFORMATION:

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TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 365 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..365
OTHER INFORMATION: /note= "Human Major Histocompatibility
CLASS I (MHC) protein"
US-08-834-497A-23

Query Match 77.1%; Score 1154; DB 3; Length 365;
Best Local Similarity 77.0%; Pred. No. 1e-104;
Matches 211; Conservative 21; Mismatches 42; Indels 0; Gaps 0;

QY 1 GSHSLRYFSTAVSRGGRGEPRYIAVEYVDDTQFLRFSDAAIPRMEPRPWPVQEGPQYW 60
DB 25 GSHSMRYFTSVSRGGRGEPRFIAVGVDYDQFVRFSDAASQRMPEPRAPWIEQEGPEYW 84

QY 61 EWTGYAKANQDTRVALNLLRRYNOSEAGSHTLQMGNGCDMPDGRLLRGYHQAIDG 120
DB 85 DGETRKVAHSQTHRVDLGTLRGYNOSEAGSHTLQMGNGCDVGSDFRFLRGYHQAIDG 144

QY 121 KDYISLNEEDLSRTAAADTVAQITQFYAEAEYAEFRYILEGECLELLRLRYLNGKETLQ 180
DB 145 KDYIALKEDLSRTAAADVAAGTTKHWEAAHVAEQRLAYLEGICVWELRYLNGKETLQ 204

QY 181 RADPPKAHVAHPISDHEATLRCWALGFYPAEITLTWQRGEGEQTQDTLVELTRPAGDGT 240
DB 205 RTDAPKTHMTTHAVSDHEATLRCWALSFPYAEITLTWQRDGEDQDTQDTLVELTRPAGDGT 264

QY 241 FOKWAAVVPVSGEQRVYCHVQHGSLPQPLILRW 274
DB 265 FOKWAAVVPVSGEQRVYCHVQHGSLPQPLILRW 298

RESULT 6
US-08-370-476-100
Sequence 100, Application US/08370476
Patent No. 6153408
GENERAL INFORMATION:
APPLICANT: Mottez, Estelle
APPLICANT: Abastado, Jean-Pierre
APPLICANT: Kourilsky, Philippe
APPLICANT: Lone, Yu-Chun
APPLICANT: Ocius, David
APPLICANT: Casrouge, Amanda
TITLE OF INVENTION: Altered Major Histocompatibility Complex
NUMBER OF SEQUENCES: 127
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESSEE: Dunner
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
STATE: D.C.
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/370,476
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:

TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 365 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCES/DOCKET NUMBER: 05243.0001-01000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 100:
SEQUENCE CHARACTERISTICS:
LENGTH: 365 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-370-476-100

Query Match 77.1%; Score 1154; DB 3; Length 365;
Best Local Similarity 76.6%; Pred. No. 1e-104;
Matches 210; Conservative 22; Mismatches 42; Indels 0; Gaps 0;

QY 1 GSHSLRYFSTAVSRGGRGEPRYIAVEYVDDTQFLRFSDAAIPRMEPRPWPVQEGPQYW 60
DB 25 GSHSMRYFTSVSRGGRGEPRFIAVGVDYDQFVRFSDAASQRMPEPRAPWIEQEGPEYW 84

QY 61 EWTGYAKANQDTRVALNLLRRYNOSEAGSHTLQMGNGCDMPDGRLLRGYHQAIDG 120
DB 85 DGETRKVAHSQTHRVDLGTLRGYNOSEAGSHTLQMGNGCDVGSDFRFLRGYHQAIDG 144

QY 121 KDYISLNEEDLSRTAAADTVAQITQFYAEAEYAEFRYILEGECLELLRLRYLNGKETLQ 180
DB 145 KDYIALKEDLSRTAAADVAAGTTKHWEAAHVAEQRLAYLEGICVWELRYLNGKETLQ 204

QY 181 RADPPKAHVAHPISDHEATLRCWALGFYPAEITLTWQRDGEDQDTQDTLVELTRPAGDGT 240
DB 205 RTDAPKTHMTTHAVSDHEATLRCWALSFPYAEITLTWQRDGEDQDTQDTLVELTRPAGDGT 264

QY 241 FOKWAAVVPVSGEQRVYCHVQHGSLPQPLILRW 274
DB 265 FOKWAAVVPVSGEQRVYCHVQHGSLPQPLILRW 298

RESULT 7
US-09-503-444A-23
Sequence 23, Application US/09503444A
Patent No. 6228594
GENERAL INFORMATION:
APPLICANT: Thomas, Winston J.
APPLICANT: Drayna, Dennis T.
APPLICANT: Feder, John N.
APPLICANT: Gnirke, Andreas
APPLICANT: Ruddy, David
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: Hereditary Hemochromatosis Gene
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect Version 8
; CURRENT APPLICATION DATA:
; EARLIER APPLICATION NUMBER: 60/021.685
; APPLICATION NUMBER: US/09/503,444A
; FILING DATE: 14-Feb-2000
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/652,265
; FILING DATE: 23-May-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/632,673
; FILING DATE: 16-Apr-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/630,912
; FILING DATE: 04-Apr-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Poissant, Brian M.
; REGISTRATION NUMBER: 28,462
; REFERENCE/DOCKET NUMBER: 8907-0088-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-9741
; TELEX: 66141
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 365 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..365
; OTHER INFORMATION: /note= "Human Major Histocompatibility
; OTHER INFORMATION: Class I (MHC) protein"
; US-09-503-444A-23

Query Match 77.1%; Score 1154; DB 3; Length 365;
Best Local Similarity 77.0%; Pred. No. 1e-104;
Matches 211; Conservative 21; Mismatches 42; Indels 0; Gaps 0;

Qy 1 GSHSLRYFSTAVSRPGRGEPRIYAEVYDDTQFLRFDSDAAIPRMEPRPWPVEQGPQYW 60
Db 25 GSHSMRYFFTSVSRPGRGEPRIYAVGYDDTQFVRFDSDAASQRMPEPRAPWIEQGPYW 84
Qy 61 EWTGYAKANAQTRVALRNLRRYNQSEAGSHTLQGMGCDMPGPRLLRGYHQHAYDG 120
Db 85 DGETRKVKAHSQTHRVDLGLTGLRGYNNQSEAGSHTLQGMGCDVGSDFLRGYHQYAYDG 144
Qy 121 KDYISLNEDLSRWTAADTVAQITQRFYEAEEYAEFRYLEGECLLRRLRYLNGKETLQ 180
Db 145 KDYIALKEDLSRWTAADTVAAQTTRKHWEAAHVAEQRLAYLGTCVWLRRLRYLNGKETLQ 204
Qy 181 RADPPKAHVHPISDHEATLRCWALGFYPAEITLTWQRDGEQTDTELVEPRAGDGT 240
Db 205 RTDAPKTHMTHAVSDHEATLRCWALSFPYPAEITLTWQRDGEQTDTELVEPRAGDGT 264
Qy 241 FQKWAAVVPSGGEQRYTCHVQHEGLPQPLIRW 274
Db 265 FQKWAAVVPSGGEQRYTCHVQHEGLPQPLIRW 298

RESULT 8
US-08-890-719-38
; Sequence 38, Application US/08890719A
; Patent No. 6075125
; GENERAL INFORMATION:
; APPLICANT: Bacon, Larry D
; APPLICANT: Hunt, Henry D
; APPLICANT: Fulton, Janet
; TITLE OF INVENTION: Production of Antisera Specific to Major
; TITLE OF INVENTION: Histocompatibility Complex Molecules in Chickens

; FILE REFERENCE: Dkt 0064.96 - Larry D. Bacon et al.
; CURRENT APPLICATION NUMBER: US/08/890,719A
; CURRENT FILING DATE: 1997-07-09
; EARLIER APPLICATION NUMBER: 60/021.685
; EARLIER FILING DATE: 1996-07-10
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 38
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-08-890-719-38

Query Match 77.1%; Score 1153; DB 3; Length 341;
Best Local Similarity 76.6%; Pred. No. 1.1e-104;
Matches 210; Conservative 22; Mismatches 42; Indels 0; Gaps 0;

Qy 1 GSHSLRYFSTAVSRPGRGEPRIYAEVYDDTQFLRFDSDAAIPRMEPRPWPVEQGPQYW 60
Db 1 GSHSMRYFFTSVSRPGRGEPRIYAVGYDDTQFVRFDSDAASQRMPEPRAPWIEQGPYW 60
Qy 61 EWTGYAKANAQTRVALRNLRRYNQSEAGSHTLQGMGCDMPGPRLLRGYHQHAYDG 120
Db 61 DGETRKVKAHSQTHRVDLGLTGLRGYNNQSEAGSHTVQRMGCDVGSDFLRGYHQYAYDG 120
Qy 121 KDYISLNEDLSRWTAADTVAQITQRFYEAEEYAEFRYLEGECLLRRLRYLNGKETLQ 180
Db 121 KDYIALKEDLSRWTAADTVAAQTTRKHWEAAHVAEQRLAYLGTCVWLRRLRYLNGKETLQ 180
Qy 181 RADPPKAHVHPISDHEATLRCWALGFYPAEITLTWQRDGEQTDTELVEPRAGDGT 240
Db 181 RTDAPKTHMTHAVSDHEATLRCWALSFPYPAEITLTWQRDGEQTDTELVEPRAGDGT 240
Qy 241 FQKWAAVVPSGGEQRYTCHVQHEGLPQPLIRW 274
Db 241 FQKWAAVVPSGGEQRYTCHVQHEGLPQPLIRW 274

RESULT 9
US-08-484-905-99
; Sequence 99, Application US/08484905
; Patent No. 5976551
; GENERAL INFORMATION:
; APPLICANT: Mottez, Estelle
; APPLICANT: Abastado, Jean-Pierre
; APPLICANT: Kourilsky, Philippe
; TITLE OF INVENTION: An Altered Major Histocompatibility
; TITLE OF INVENTION: Complex (MHC) Determinant and Methods for Using the
; NUMBER OF SEQUENCES: 127
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Parabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W., Suite 700
; CITY: Washington
; STATE: D.C.
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS-/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,905
; FILING DATE: 07-JUNE-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/801,818
; FILING DATE: 05-DEC-1991
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/792,473
; FILING DATE: 15-NOV-1991
```

```

; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Potter, Jane E. R.
; REGISTRATION NUMBER: 33,332
; REFERENCE/DOCKET NUMBER: 03495.0106-03000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 99:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 365 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-484-905-99

Query Match 76.9%; Score 1151; DB 2; Length 365;
Best Local Similarity 76.3%; Pred. No. 2e-104;
Matches 209; Conservative 23; Mismatches 42; Indels 0; Gaps 0;

Qy 1 GSHSLRVSTAVSRPGCEPRYIAVYVDDTQFLRFSDAAIPRMEPREPWVEQGPQYW 60
Db 25 GSHSMRYFTSVSRPGCEPRFIAGVYDDTQFVRFSDAASQRMPEPRAPWIEQGPY 84
Qy 61 EWTGYAKANAQTRVALNRLRRYNSQAGSHTLQMGNGCDMGPDGRLLRGYHQYADG 120
Db 85 DGETRKVAHSQTHRVLDLTLRGYYNSQAGSHTVQRMVYCDVSGDGRFLRGYHQYADG 144
Qy 121 KDYISLNDLASWTAADTVAQITQRYEAEVEAEFRYLEGECLELLRLRYLENGKETLQ 180
Db 145 KDYLAKEDLASWTAADMAAQTTKHKEAHEAQWRAYLEGTCVEMRLRYLENGKETLQ 204
Qy 181 RADPPKAHVAHPISDHEATLRCWALGFYPAEITLTWQDGEBOQDTDELVETRPAGDGT 240
Db 205 RTDAPKTHMTHAVSDHEATLRCWALSFPYAEITLTWQDGEDQTDQDELVETRPAGDGT 264
Qy 241 FQKWAUVVPSGEGORYTCHVQHEGLPQLILRW 274
Db 265 FQKWAUVVPSGEGORYTCHVQHEGLPKPLTLPLW 298

RESULT 10
US-08-484-905-104
; Sequence 104, Application US/08484905
; Patent No. 5976551
; GENERAL INFORMATION:
; APPLICANT: Mottez, Estelle
; APPLICANT: Abastado, Jean-Pierre
; APPLICANT: Kourilsky, Philippe
; TITLE OF INVENTION: An Altered Major Histocompatibility
; TITLE OF INVENTION: Complex (MHC) Determinant and Methods for Using the
; TITLE OF INVENTION: Determinant
; NUMBER OF SEQUENCES: 127
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; STREET: 1300 I Street, N.W., Suite 700
; CITY: Washington
; STATE: D.C.
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS-/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,905
; FILING DATE: 07-JUNE-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/801,818
; FILING DATE: 03-DEC-1991
; CLASSIFICATION: 530

; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Potter, Jane E. R.
; REGISTRATION NUMBER: 33,332
; REFERENCE/DOCKET NUMBER: 03495.0106-03000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 99:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 365 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-484-905-104

Query Match 76.9%; Score 1151; DB 2; Length 365;
Best Local Similarity 76.3%; Pred. No. 2e-104;
Matches 209; Conservative 23; Mismatches 42; Indels 0; Gaps 0;

Qy 1 GSHSLRVSTAVSRPGCEPRYIAVYVDDTQFLRFSDAAIPRMEPREPWVEQGPQYW 60
Db 25 GSHSMRYFTSVSRPGCEPRFIAGVYDDTQFVRFSDAASQRMPEPRAPWIEQGPY 84
Qy 61 EWTGYAKANAQTRVALNRLRRYNSQAGSHTLQMGNGCDMGPDGRLLRGYHQYADG 120
Db 85 DGETRKVAHSQTHRVLDLTLRGYYNSQAGSHTVQRMVYCDVSGDGRFLRGYHQYADG 144
Qy 121 KDYISLNDLASWTAADTVAQITQRYEAEVEAEFRYLEGECLELLRLRYLENGKETLQ 180
Db 145 KDYLAKEDLASWTAADMAAQTTKHKEAHEAQWRAYLEGTCVEMRLRYLENGKETLQ 204
Qy 181 RADPPKAHVAHPISDHEATLRCWALGFYPAEITLTWQDGEBOQDTDELVETRPAGDGT 240
Db 205 RTDAPKTHMTHAVSDHEATLRCWALSFPYAEITLTWQDGEDQTDQDELVETRPAGDGT 264
Qy 241 FQKWAUVVPSGEGORYTCHVQHEGLPQLILRW 274
Db 265 FQKWAUVVPSGEGORYTCHVQHEGLPKPLTLPLW 298

RESULT 11
US-08-481-985B-99
; Sequence 99, Application US/08481985B
; Patent No. 6011146
; GENERAL INFORMATION:
; APPLICANT: Mottez, Estelle
; APPLICANT: Abastado, Jean-Pierre
; APPLICANT: Kourilsky, Philippe
; TITLE OF INVENTION: Altered Major Histocompatibility Complex
; TITLE OF INVENTION:
; NUMBER OF SEQUENCES: 148
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; STREET: 1300 I Street, N.W., Suite 700
; CITY: Washington
; STATE: D.C.
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/481,985B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/801,818
; FILING DATE: 03-DEC-1991
; CLASSIFICATION: 530
```

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; FILING DATE: 05-DEC-1991
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/792,473
; FILING DATE: 15-NOV-1991
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 03495.0106-04000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4400
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 99:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 365 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-481-985B-99

Query Match 76.9%; Score 1151; DB 3; Length 365;
Best Local Similarity 76.3%; Pred. No. 2e-104;
Matches 209; Conservative 23; Mismatches 42; Indels 0; Gaps 0;

QY 1 GSHSLRYFSTAVSRPGRGEPYIAVYVDDTQFLRFDSDAAIPRMEPRFPWVEQGPQYW 60
DB 25 GSHSMRYFTSVSRPGRGEPYIAVGYVDDTQFVRFSDAASQRMPEPRAPWIEQGPYW 84
QY 61 EWTGAKANAQTRVALRNLRLRYNQSEAGSHLQMGNCMDGPDGRLRGYHQHAYDG 120
DB 85 DGETRKYKAHSQTHRVLDLSTLRGYNQSEAGSHVQMTGYCDVGSDFRLRGYHQHAYDG 144
QY 121 KDVISLNEDELRSTAAADTVAQITQRFYEAEBEYAEFEFTYLEGCLELLRLRYLENGKETLQ 180
DB 145 KDVIALKEDLSRWTRADMAAQTTHKWEAHEAQWRAYLEGTCVWLRLRYLENGKETLQ 204
QY 181 RADPPKAHVHPISDHEATLRCWALGYPAEITLTWQRDGEQOTQDTLVELTRPAGDGT 240
DB 205 RTDAPKTHMTHAVSDHEATLRCWALSFPYPAEITLTWQRDGEQOTQDTLVELTRPAGDGT 264
QY 241 FOKWAAVVVPSGGEORYTCHVQHEGLPOPLILRW 274
DB 265 FOKWAAVVVPSGGEORYTCHVQHEGLPKPLTLFW 298

RESULT 12
; Sequence 104, Application US/08481985B
; Patent No. 601146
; GENERAL INFORMATION:
; APPLICANT: Mottez, Estelle
; APPLICANT: Abastado, Jean-Pierre
; APPLICANT: Kourilsky, Philippe
; TITLE OF INVENTION: Altered Major Histocompatibility Complex
; TITLE OF INVENTION:
; NUMBER OF SEQUENCES: 148
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; STREET: 1300 I Street, N.W., Suite 700
; CITY: Washington
; STATE: D.C.
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/481.985B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/801,818
; FILING DATE: 05-DEC-1991
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/792,473
; FILING DATE: 15-NOV-1991
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 03495.0106-04000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4400
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 104:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 365 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-481-985B-104

Query Match 76.9%; Score 1151; DB 3; Length 365;
Best Local Similarity 76.3%; Pred. No. 2e-104;
Matches 209; Conservative 22; Mismatches 43; Indels 0; Gaps 0;

QY 1 GSHSLRYFSTAVSRPGRGEPYIAVYVDDTQFLRFDSDAAIPRMEPRFPWVEQGPQYW 60
DB 25 GSHSMRYFTSVSRPGRGEPYIAVGYVDDTQFVRFSDAASQRMPEPRAPWIEQGPYW 84
QY 61 EWTGAKANAQTRVALRNLRLRYNQSEAGSHLQMGNCMDGPDGRLRGYHQHAYDG 120
DB 85 DFNTENVAQSQTRVDLSTLRGYNQSEAGSHVQMTGYCDVGSDFRLRGYRODAYDG 144
QY 121 KDVISLNEDELRSTAAADTVAQITQRFYEAEBEYAEFEFTYLEGCLELLRLRYLENGKETLQ 180
DB 145 KDVIALKEDLSRWTRADMAAQTTHKWEAHEAQWRAYLEGTCVWLRLRYLENGKETLQ 204
QY 181 RADPPKAHVHPISDHEATLRCWALGYPAEITLTWQRDGEQOTQDTLVELTRPAGDGT 240
DB 205 RTDAPKTHMTHAVSDHEATLRCWALSFPYPAEITLTWQRDGEQOTQDTLVELTRPAGDGT 264
QY 241 FOKWAAVVVPSGGEORYTCHVQHEGLPOPLILRW 274
DB 265 FOKWAAVVVPSGGEORYTCHVQHEGLPKPLTLFW 298

RESULT 13
; Sequence 99, Application US/08370476
; Patent No. 6153408
; GENERAL INFORMATION:
; APPLICANT: Mottez, Estelle
; APPLICANT: Abastado, Jean-Pierre
; APPLICANT: Kourilsky, Philippe
; APPLICANT: Lone, Yu-Chun
; APPLICANT: Ojcius, David
; APPLICANT: Casrouge, Armanda
; TITLE OF INVENTION: Altered Major Histocompatibility Complex
; TITLE OF INVENTION:
; NUMBER OF SEQUENCES: 127
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; STREET: 1300 I Street, N.W., Suite 700
; CITY: Washington
; STATE: D.C.
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

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/ TITLE OF INVENTION: Complex(MHC) Determinant and Methods for Using the
/ TITLE OF INVENTION: Determinant
/ NUMBER OF SEQUENCES: 127
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
/ ADDRESSEE: Dunner
/ STREET: 1300 I Street, N.W., Suite 700
/ CITY: Washington
/ STATE: D.C.
/ ZIP: 20005-3315
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy Disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS-/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/484,905
/ FILING DATE: 07-JUNE-1995
/ CLASSIFICATION: 530
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/801,818
/ FILING DATE: 05-DEC-1991
/ CLASSIFICATION: 530
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/792,473
/ FILING DATE: 15-NOV-1991
/ CLASSIFICATION: 530
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Potter, Jane E. R.
/ REGISTRATION NUMBER: 33,332
/ REFERENCE/DOCKET NUMBER: 03495.0106-03000
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 202-408-4000
/ TELEFAX: 202-408-4400
/ INFORMATION FOR SEQ ID NO: 107:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 274 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ US-08-484-905-107

Query Match 76.9%; Score 1150; DB 2; Length 274;
Best Local Similarity 76.6%; Pred. No. 1.7e-104;
Matches 210; Conservative 22; Mismatches 42; Indels 0; Gaps 0;

Qy	1	GSHSLRYFTAVSRPGRGPRYIAVYVDDTQFLRFDSDAAIPRMEPRPWPVEQSGPQYW	60
Db	1	GSHSMRYFFTSVSRPGRGPRFTIAGYVDDTQVRFDSDAASRRMEPRAPWIEQSGPEYW	60
Qy	61	EWTTGYAKANAQTDYVALNLLRRYVNSAGSHTLQGMNGCDMPDGRLLRGVHGHAYDG	120
Db	61	DGSTRKVKAKSQTHRVLDLSTLRGYVNSAGSHTLQGMNGCDVGSDFRFLRGVHGHAYDG	120
Qy	121	KDYISLNEDLRSWTAADTVAQTQRFYAEAEFEPTYLEGCELELLRRYLENGKETLQ	180
Db	121	KDYIALKEDLRSWTAADMAAQTTHKWEAAHVAEQWRAYLEGTCVWLSRYLENGKETLQ	180
Qy	181	RADPPKAHVAHPISEHATLRCWALGFYPABITLTWQDGEQDQDTDELVETRPAGDGT	240
Db	181	RTDAPKTHMTHAVSDEHATLRCWALGFYPABITLTWQDGEDQDQDTDELVETRPAGDGT	240
Qy	241	FOKWAAVVVPSSGEQRYTCHVQHEGLPQPLILRW	274
Db	241	FOKWAAVVVPSSGEQRYTCHVQHEGLPKPLTLPW	274

Search completed: June 18, 2004, 19:28:39
Job time : 23 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 18, 2004, 19:18:00 ; Search time 50 Seconds  
(without alignments)  
1547.079 Million cell updates/sec

Title: US-09-819-371-5  
Perfect score: 1496  
Sequence: 1 GSHSLRYFSTAVSRGRGEP.....QRYTCHVQHGLPQLILRW 274

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1163542 seqs, 282313646 residues

Total number of hits satisfying chosen parameters: 1163542

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA:\*  
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2: /cgn2\_6/prodata/2/pubpaa/PCT\_NEW\_PUB.pcp:\*  
3: /cgn2\_6/prodata/2/pubpaa/US05\_NEW\_PUB.pcp:\*  
4: /cgn2\_6/prodata/2/pubpaa/US06\_PUBCOMB.pcp:\*  
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10: /cgn2\_6/prodata/2/pubpaa/US09B\_PUBCOMB.pcp:\*  
11: /cgn2\_6/prodata/2/pubpaa/US09C\_PUBCOMB.pcp:\*  
12: /cgn2\_6/prodata/2/pubpaa/US09D\_PUBCOMB.pcp:\*  
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14: /cgn2\_6/prodata/2/pubpaa/US10B\_PUBCOMB.pcp:\*  
15: /cgn2\_6/prodata/2/pubpaa/US10C\_PUBCOMB.pcp:\*  
16: /cgn2\_6/prodata/2/pubpaa/US10D\_PUBCOMB.pcp:\*  
17: /cgn2\_6/prodata/2/pubpaa/US10E\_PUBCOMB.pcp:\*  
18: /cgn2\_6/prodata/2/pubpaa/US10F\_PUBCOMB.pcp:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1496	100.0	274	12	US-09-819-371-5
2	1496	100.0	362	12	US-10-257-021-82
3	1496	100.0	442	16	US-10-408-765A-1887
4	1489	99.5	362	12	US-09-819-371-4
5	1311	87.6	271	9	US-09-925-301-1431
6	1184	79.1	326	12	US-10-380-880-7
7	1174.5	78.5	379	12	US-10-210-172-160
8	1174.5	78.5	379	15	US-10-093-463-78
9	1164	77.8	215	12	US-09-819-371-6
10	1158	77.4	364	15	US-10-093-463-80
11	1154	77.1	365	14	US-10-138-888-23
12	1153	77.1	280	14	US-10-073-300-6
13	1153	77.1	280	16	US-10-075-257-6
14	1153	77.1	415	14	US-10-073-300-5
15	1153	77.1	415	16	US-10-075-257-5

16	1153	77.1	510	12	US-10-108-511-5	Sequence 5, Appli
17	1133.5	75.8	389	12	US-10-108-511-2	Sequence 2, Appli
18	1131	75.6	371	12	US-10-210-172-156	Sequence 156, App
19	1131	75.6	371	15	US-10-085-198-72	Sequence 72, Appl
20	1098.5	73.4	452	12	US-10-210-172-152	Sequence 152, App
21	1098.5	73.4	452	15	US-10-085-198-68	Sequence 68, Appl
22	1097	73.3	361	14	US-10-138-888-22	Sequence 22, Appl
23	1070.5	71.6	389	15	US-10-085-198-70	Sequence 70, Appl
24	1066	71.3	421	12	US-10-210-172-174	Sequence 174, App
25	1066	71.3	421	15	US-10-138-588-32	Sequence 32, Appl
26	1010	67.5	540	14	US-10-015-535-22	Sequence 22, Appl
27	1010	67.5	541	14	US-10-015-535-28	Sequence 28, Appl
28	1010	67.5	542	14	US-10-015-535-24	Sequence 24, Appl
29	1010	67.5	542	14	US-10-015-535-26	Sequence 26, Appl
30	1010	67.5	542	14	US-10-015-535-32	Sequence 32, Appl
31	1010	67.5	542	14	US-10-015-535-34	Sequence 34, Appl
32	1005	67.2	542	14	US-10-015-535-36	Sequence 36, Appl
33	1002	67.0	540	14	US-10-015-535-30	Sequence 30, Appl
34	930	62.2	256	16	US-10-408-765A-247	Sequence 247, App
35	832	55.6	284	15	US-10-104-047-3648	Sequence 3648, Ap
36	773	51.7	234	12	US-10-380-880-8	Sequence 8, Appli
37	771	51.5	201	15	US-10-264-049-4199	Sequence 4199, Ap
38	724	48.4	184	9	US-09-858-580-21	Sequence 21, Appl
39	724	48.4	184	10	US-09-847-172-21	Sequence 21, Appl
40	689	46.1	181	10	US-09-013-077A-13	Sequence 13, Appl
41	580	38.8	145	9	US-09-810-560-8	Sequence 8, Appli
42	570	38.1	196	12	US-10-262-839-48	Sequence 48, Appl
43	526	35.2	341	15	US-10-143-822-1	Sequence 1, Appli
44	513	34.3	96	14	US-10-029-386-30718	Sequence 30718, A
45	510	34.1	332	9	US-09-870-521-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1  
US-09-819-371-5  
; Sequence 5, Application US/09819371  
; Publication No. US20040053344A1  
; GENERAL INFORMATION:  
; APPLICANT: Egawa, Kohji  
; TITLE OF INVENTION: Cancer Cell-Specific HLA-F Antigen and a Diagnostic Method of Ca  
; FILE REFERENCE: 30815  
; CURRENT APPLICATION NUMBER: US/09/819,371  
; CURRENT FILING DATE: 2002-03-15  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 5  
; LENGTH: 274  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-819-371-5

Query Match 100.0%; Score 1496; DB 12; Length 274;  
Best Local Similarity 100.0%; Pred. No. 2.6e-140; Indels 0; Gaps 0;  
Matches 274; Conservative 0; Mismatches 0;

Qy	1	GSHSLRYFSTAVSRGRGEPYIAVEYVDDTQFLRFDSDAAIPRMEPREPWVEGPOYW	60
Db	1	GSHSLRYFSTAVSRGRGEPYIAVEYVDDTQFLRFDSDAAIPRMEPREPWVEGPOYW	60
Qy	61	EWTGTYAKANAQTRVALNRLRLRYNSEAGSHYLOQNGCDMGPDGRLLYGHQYHAYDG	120
Db	61	EWTGTYAKANAQTRVALNRLRLRYNSEAGSHYLOQNGCDMGPDGRLLYGHQYHAYDG	120
Qy	121	KDYISLNEDLSWTAADTVAQITQFYAEABYAEFFRYLGECELELLRRLYLENGKETLO	180
Db	121	KDYISLNEDLSWTAADTVAQITQFYAEABYAEFFRYLGECELELLRRLYLENGKETLO	180
Qy	181	RADPPKAVHAHPISDHEATLRCWALGFYPABITLTWQDGEETQDTETELVETRPAGDGT	240
Db	181	RADPPKAVHAHPISDHEATLRCWALGFYPABITLTWQDGEETQDTETELVETRPAGDGT	240

QY 241 FOKWAAVVVPSGGEQRYTCHVQHEGLPQPLILRW 274  
DB 241 FOKWAAVVVPSGGEQRYTCHVQHEGLPQPLILRW 274

## RESULT 2

US-10-257-021-82  
; Sequence 82, Application US/10257021  
; Publication No. US20030211498A1  
; GENERAL INFORMATION:  
; APPLICANT: Morin, Patrice J.  
; APPLICANT: Sherman-Baust, Cheryl A.  
; APPLICANT: Pizer, Ellen S.  
; APPLICANT: Hough, Colleen D.  
; TITLE OF INVENTION: TUMOR MARKERS IN OVARIAN CANCER  
; FILE REFERENCE: 14014.0369U2  
; CURRENT APPLICATION NUMBER: US/10/257,021  
; CURRENT FILING DATE: 2002-10-03  
; PRIOR FILING DATE: 2001-04-03  
; PRIOR APPLICATION NUMBER: 60/194,336  
; PRIOR FILING DATE: 2000-04-03  
; NUMBER OF SEQ ID NOS: 147  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 82  
; LENGTH: 362  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-257-021-82

Query Match 100.0%; Score 1496; DB 12; Length 362;  
Best Local Similarity 100.0%; Pred. No. 3.8e-140;  
Matches 274; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSHSLRYFSTAVSRPGRGEPYIAVEYVDDTQFLRFDSDAAIPRMEPRPWEQSGPQYW 60  
DB 22 GSHSLRYFSTAVSRPGRGEPYIAVEYVDDTQFLRFDSDAAIPRMEPRPWEQSGPQYW 81  
QY 61 EWTGAKANAQTDRAVALNRLRRYNSQAGSHTLQGMNCGDMPDGRLLRGYHAYDG 120  
DB 82 EWTGAKANAQTDRAVALNRLRRYNSQAGSHTLQGMNCGDMPDGRLLRGYHAYDG 141  
QY 121 KDYSILNEDLSRWTAAADTVAQITQRFYAEAEYAEFFTYLEGECELELLRRYLENGKETLQ 180  
DB 142 KDYSILNEDLSRWTAAADTVAQITQRFYAEAEYAEFFTYLEGECELELLRRYLENGKETLQ 201  
QY 181 RADPPKAHVAHPISDHEATLRCWALGFYPABITLTTWQRDGEEQTDTELVTETRPAGDGT 240  
DB 202 RADPPKAHVAHPISDHEATLRCWALGFYPABITLTTWQRDGEEQTDTELVTETRPAGDGT 261  
QY 241 FOKWAAVVVPSGGEQRYTCHVQHEGLPQPLILRW 274  
DB 262 FOKWAAVVVPSGGEQRYTCHVQHEGLPQPLILRW 295

## RESULT 3

US-10-408-765A-1887  
; Sequence 1887, Application US/10408765A  
; Publication No. US20040101874A1  
; GENERAL INFORMATION:  
; APPLICANT: Ghosh, Soumitra S.  
; APPLICANT: Fahy, Eoin D.  
; APPLICANT: Zhang, Bing  
; APPLICANT: Gibson, Bradford W.  
; APPLICANT: Taylor, Steven W.  
; APPLICANT: Glenn, Gary M.  
; APPLICANT: Warnock, Dale E.  
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION  
; FILE REFERENCE: 660088.465  
; CURRENT APPLICATION NUMBER: US/10/408,765A  
; CURRENT FILING DATE: 2003-04-04

; NUMBER OF SEQ ID NOS: 3077  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1887  
; LENGTH: 442  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-408-765A-1887

Query Match 100.0%; Score 1496; DB 16; Length 442;  
Best Local Similarity 100.0%; Pred. No. 4.9e-140;  
Matches 274; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSHSLRYFSTAVSRPGRGEPYIAVEYVDDTQFLRFDSDAAIPRMEPRPWEQSGPQYW 60  
DB 22 GSHSLRYFSTAVSRPGRGEPYIAVEYVDDTQFLRFDSDAAIPRMEPRPWEQSGPQYW 81  
QY 61 EWTGAKANAQTDRAVALNRLRRYNSQAGSHTLQGMNCGDMPDGRLLRGYHAYDG 120  
DB 82 EWTGAKANAQTDRAVALNRLRRYNSQAGSHTLQGMNCGDMPDGRLLRGYHAYDG 141  
QY 121 KDYSILNEDLSRWTAAADTVAQITQRFYAEAEYAEFFTYLEGECELELLRRYLENGKETLQ 180  
DB 142 KDYSILNEDLSRWTAAADTVAQITQRFYAEAEYAEFFTYLEGECELELLRRYLENGKETLQ 201  
QY 181 RADPPKAHVAHPISDHEATLRCWALGFYPABITLTTWQRDGEEQTDTELVTETRPAGDGT 240  
DB 202 RADPPKAHVAHPISDHEATLRCWALGFYPABITLTTWQRDGEEQTDTELVTETRPAGDGT 261  
QY 241 FOKWAAVVVPSGGEQRYTCHVQHEGLPQPLILRW 274  
DB 262 FOKWAAVVVPSGGEQRYTCHVQHEGLPQPLILRW 295

## RESULT 4

US-09-819-371-4  
; Sequence 4, Application US/09819371  
; Publication No. US2004005344A1  
; GENERAL INFORMATION:  
; APPLICANT: Egawa, Kohji  
; TITLE OF INVENTION: Cancer Cell-Specific HLA-F Antigen and a Diagnostic Method of C.  
; FILE REFERENCE: 30815  
; CURRENT APPLICATION NUMBER: US/09/819,371  
; CURRENT FILING DATE: 2002-03-15  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 4  
; LENGTH: 362  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-819-371-4

Query Match 99.5%; Score 1489; DB 12; Length 362;  
Best Local Similarity 99.6%; Pred. No. 1.9e-139;  
Matches 273; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GSHSLRYFSTAVSRPGRGEPYIAVEYVDDTQFLRFDSDAAIPRMEPRPWEQSGPQYW 60  
DB 22 GSHSLRYFSTAVSRPGRGEPYIAVEYVDDTQFLRFDSDAAIPRMEPRPWEQSGPQYW 81  
QY 61 EWTGAKANAQTDRAVALNRLRRYNSQAGSHTLQGMNCGDMPDGRLLRGYHAYDG 120  
DB 82 EWTGAKANAQTDRAVALNRLRRYNSQAGSHTLQGMNCGDMPDGRLLRGYHAYDG 141  
QY 121 KDYSILNEDLSRWTAAADTVAQITQRFYAEAEYAEFFTYLEGECELELLRRYLENGKETLQ 180  
DB 142 KDYSILNEDLSRWTAAADTVAQITQRFYAEAEYAEFFTYLEGECELELLRRYLENGKETLQ 201  
QY 181 RADPPKAHVAHPISDHEATLRCWALGFYPABITLTTWQRDGEEQTDTELVTETRPAGDGT 240  
DB 202 RADPPKAHVAHPISDHEATLRCWALGFYPABITLTTWQRDGEEQTDTELVTETRPAGDGT 261  
QY 241 FOKWAAVVVPSGGEQRYTCHVQHEGLPQPLILRW 274

Db 262 FQWAAVVPVSGEQRYTCHVQHEGLPQPLILRW 295  
|||||  
RESULT 5  
US-09-925-301-1431  
; Sequence 1431, Application US/09925301  
; Patent No. US20020052308A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies  
; FILE REFERENCE: PA106  
; CURRENT APPLICATION NUMBER: US/09/925,301  
; PRIOR FILING DATE: 2001-08-10  
; PRIOR APPLICATION NUMBER: PCT/US00/05882  
; PRIOR FILING DATE: 2000-03-08  
; PRIOR APPLICATION NUMBER: 60/124,270  
; PRIOR FILING DATE: 1999-03-12  
; NUMBER OF SEQ ID NOS: 1694  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1431  
; LENGTH: 271  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-925-301-1431  
Query Match 87.6%; Score 1311; DB 9; Length 271;  
Best Local Similarity 99.6%; Pred. No. 6.5e-122;  
Matches 241; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GSHSLRYFSTAVSRPGRGEPRIYAVYVDDTQFLRFDSDAAIPRMEPREPFWVEQGPQYW 60  
DB 28 GSHSLRYFSTAVSRPGRGEPRIYAVYVDDTQFLRFDSDAAIPRMEPREPFWVEQGPQYW 87  
QY 61 EWTTCYAKANAQDRVALNRLRRYNQSEAGSHTLQWNGCDMPDGRLLRGVHQHAYDG 120  
DB 88 EWTTCYAKANAQDRVALNRLRRYNQSEAGSHTLQWNGCDMPDGRLLRGVHQHAYDG 147  
QY 121 KQYISLNEDLSRWSAATVAQITQRTYEAEBYAEFFRTYLEGECLELLRRLRYLENGKETIQ 180  
DB 148 KQYISLNEDLSRWSAATVAQITQRTYEAEBYAEFFRTYLEGECLELLRRLRYLENGKETIQ 207  
QY 181 RADPPKAAVHAHPISDHEATLRCWALGFYPAEITLTWQDGBEOTDTVELVETRPAGDGT 240  
DB 208 RADPPKAAVHAHPISDHEATLRCWALGFYPAEITLTWQDGBEOTDTVELVETRPAGDGT 267  
QY 241 FQ 242  
DB 268 FR 269  
RESULT 6  
US-10-380-880-7  
; Sequence 7, Application US/10380880  
; Publication No. US20040044182A1  
; GENERAL INFORMATION:  
; APPLICANT: Hunt, Joan S.  
; APPLICANT: Morales, Pedro J.  
; APPLICANT: Petroff, Margaret G.  
; TITLE OF INVENTION: EXPRESSION, PREPARATION, USES, AND SEQUENCE OF RECOMBINANTLY-DERIVED  
; TITLE OF INVENTION: SOLUBLE HLA-G  
; FILE REFERENCE: Docket No. US20040044182A1 30772  
; CURRENT APPLICATION NUMBER: US/10/380,880  
; CURRENT FILING DATE: 2003-03-17  
; PRIOR APPLICATION NUMBER: US 60/232,761  
; PRIOR FILING DATE: 2000-09-15  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 7  
; LENGTH: 326  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-380-880-7

Query Match 79.1%; Score 1184; DB 12; Length 326;  
Best Local Similarity 78.8%; Pred. No. 3.7e-109;  
Matches 216; Conservative 22; Mismatches 36; Indels 0; Gaps 0;  
QY 1 GSHSLRYFSTAVSRPGRGEPRIYAVYVDDTQFLRFDSDAAIPRMEPREPFWVEQGPQYW 60  
DB 32 GSHSLRYFSTAVSRPGRGEPRIYAVYVDDTQFLRFDSDAAIPRMEPREPFWVEQGPQYW 91  
QY 61 EWTTCYAKANAQDRVALNRLRRYNQSEAGSHTLQWNGCDMPDGRLLRGVHQHAYDG 120  
DB 92 EETRTKAAHAQTDRLNLTQTLRGYNNQSEASHTLQWNGCDMPDGRLLRGVHQHAYDG 151  
QY 121 KQYISLNEDLSRWSAATVAQITQRTYEAEBYAEFFRTYLEGECLELLRRLRYLENGKETIQ 180  
DB 152 KQYISLNEDLSRWSAATVAQITQRTYEAEBYAEFFRTYLEGECLELLRRLRYLENGKETIQ 211  
QY 181 RADPPKAAVHAHPISDHEATLRCWALGFYPAEITLTWQDGBEOTDTVELVETRPAGDGT 240  
DB 212 RADPPKAAVHAHPISDHEATLRCWALGFYPAEITLTWQDGBEOTDTVELVETRPAGDGT 271  
QY 241 FQWAAVVPVSGEQRYTCHVQHEGLPQPLILRW 274  
DB 272 FQWAAVVPVSGEQRYTCHVQHEGLPQPLILRW 305  
RESULT 7  
US-10-210-172-160  
; Sequence 160, Application US/10210172  
; Publication No. US20040043928A1  
; GENERAL INFORMATION:  
; APPLICANT: Kekuda, Ramesh  
; APPLICANT: Miller, Charles  
; APPLICANT: Patturajan, Meera  
; APPLICANT: Pena, Carol  
; APPLICANT: Rieger, Daniel  
; APPLICANT: Shinkets, Richard  
; APPLICANT: Zerkusen, Bryan  
; APPLICANT: Li, Li  
; APPLICANT: Ji, Weizhen  
; APPLICANT: Padigaru, Muralidhara  
; APPLICANT: Casman, Stacie  
; APPLICANT: Voss, Edward  
; APPLICANT: Boldog, Ferenc  
; APPLICANT: Gorman, Linda  
; APPLICANT: Leite, Mario  
; APPLICANT: Vernet, Corine  
; APPLICANT: Anderson, David  
; APPLICANT: Guo, Xiaojia  
; APPLICANT: Zhong, Mei  
; APPLICANT: Gerlach, Valerie  
; APPLICANT: Hjalte, Tord  
; APPLICANT: Rastelli, Luca  
; APPLICANT: Spytek, Kimberly  
; APPLICANT: Edinger, Shlomit  
; APPLICANT: Ellerman, Karen  
; APPLICANT: Malyankar, Uriel  
; APPLICANT: MacDougall, John  
; APPLICANT: Stone, David  
; APPLICANT: Alsobrook II, John  
; APPLICANT: Lepley, Denise et al.  
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD  
; FILE REFERENCE: 21402-416 A  
; CURRENT APPLICATION NUMBER: US/10/210,172  
; CURRENT FILING DATE: 2001-08-01  
; PRIOR APPLICATION NUMBER: 60/309,501  
; PRIOR FILING DATE: 2001-08-02  
; PRIOR APPLICATION NUMBER: 60/323,994  
; PRIOR FILING DATE: 2001-09-21  
; PRIOR APPLICATION NUMBER: 60/373,814  
; PRIOR FILING DATE: 2002-04-19  
; PRIOR APPLICATION NUMBER: 60/310,291  
; PRIOR FILING DATE: 2001-08-03

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; PRIOR APPLICATION NUMBER: 60/310,951
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/310,544
; PRIOR FILING DATE: 2001-08-07
; PRIOR APPLICATION NUMBER: 60/311,292
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 60/311,979
; PRIOR FILING DATE: 2001-08-13
; PRIOR APPLICATION NUMBER: 60/313,201
; PRIOR FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 60/312,892
; PRIOR FILING DATE: 2001-08-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 327
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 160
; LENGTH: 379
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-210-172-160

Query Match      78.5%; Score 1174.5; DB 12; Length 379;
Best Local Similarity 78.0%; Pred. No. 4e-108;
Matches 216; Conservative 22; Mismatches 36; Indels 3; Gaps 1;

QY 1 GSHSLRYPSTAVSRPGGEPRYIAVEYVDDTQFLRFDSDAAIPRMEPRPWPVEQGPYW 60
DB 25 GSHSNRYFSAVSRPGGEPRFIAMGYVDDTQFVRFDSDSACPRMEPRAPWVEQGPYW 84
QY 61 EWTGTGAKANAQTRVALNRLNRYNOSEA---GSHTLQMGNGCDMGDPGRLLRGVHOA 117
DB 85 EESTRNTKAAQTRDMNLQTLRGYNQSGVPGSGHTLQWMTGCDLGS DGRLLRGYEQYA 144
QY 118 YDGDYISLNE DLRSWTAADTVAQITQFYBAEYABEFRTYLRGECLELLRRYLENGKE 177
DB 145 YDGRDYALNEDLRSWTAADTAAQISKRKCEANVAEQRRAYLGSTCVEMHLRYLENGKE 204
QY 178 TLQRADPPKAVHHPHSIDHEATRLCWALGYPAEITLTWDRDGEQOTDTLVETRPAG 237
DB 205 MLQRADPPKTHVTHHPVDYEATRLCWALGYPAEITLTWDRDGEQOTDTLVETRPAG 264
QY 238 DGTQKAAVVPVSGEGRYCHVQHEGLPOPLLRW 274
DB 265 DGTQKAAVVPVSGEGRYCHVQHEGLPFLMLRW 301

RESULT 8
US-10-093-463-78
; Sequence 78, Application US/10093463
; Publication No. US20030208039A1
; GENERAL INFORMATION:
; APPLICANT: Padigar, Muralidhara
; APPLICANT: Shenoy, Suresh
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Gusev, Vladimir
; APPLICANT: Pochart, Pascal
; APPLICANT: Zhong, Mei
; APPLICANT: Rastelli, Luca
; APPLICANT: Mezes, Peter
; APPLICANT: Smithson, Glenda
; APPLICANT: Guo, Xiaojia
; APPLICANT: Gexlach, Valerie
; APPLICANT: Casman, Stacie
; APPLICANT: Boldog, Ferenc
; APPLICANT: Li, Li
; APPLICANT: Zethusen, Bryan
; APPLICANT: Tchernev, Velizar
; APPLICANT: Gangolli, Esha
; APPLICANT: Vernet, Corine
; APPLICANT: Pena, Carol
; APPLICANT: Burgess, Catherine
; APPLICANT: Liu, Xiaohong
; APPLICANT: Spytek, Kimberly
```

```
; APPLICANT: Gorman, Linda
; APPLICANT: Spaderna, Steven
; APPLICANT: Voss, Edward
; APPLICANT: Malyankar, Uriel
; APPLICANT: Anderson, David
; APPLICANT: Patturajan, Meera
; APPLICANT: Miller, Charles
; APPLICANT: Taupier, Raymond J. Jr.
; TITLE OF INVENTION: No. US20030208039A1el Antibodies that Bind to Antigenic Polypep
; FILE OF INVENTION: Encoding The Antigens, and Methods of Use.
; FILE REFERENCE: 21402-290A (Cura 590AT)
; CURRENT APPLICATION NUMBER: US/10/093,463
; CURRENT FILING DATE: 2002-06-24
; PRIOR APPLICATION NUMBER: 60/283,675
; PRIOR FILING DATE: 2001-04-14
; PRIOR APPLICATION NUMBER: 60/338,092
; PRIOR FILING DATE: 2001-12-03
; PRIOR APPLICATION NUMBER: 60/274,281
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: 60/274,101
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: 60/325,681
; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: 60/304,354
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/279,995
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 60/294,899
; PRIOR FILING DATE: 2001-05-31
; PRIOR APPLICATION NUMBER: 60/287,424
; PRIOR FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: 60/299,027
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 60/309,198
; PRIOR FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: 60/281,194
; PRIOR FILING DATE: 2001-04-04
; PRIOR APPLICATION NUMBER: 60/274,194
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: 60/274,849
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/330,380
; PRIOR FILING DATE: 2001-10-18
; PRIOR APPLICATION NUMBER: 60/275,235
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: 60/288,342
; PRIOR FILING DATE: 2001-05-03
; PRIOR APPLICATION NUMBER: 60/275,578
; PRIOR FILING DATE: 2001-03-13
; NUMBER OF SEQ ID NOS: 370
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 78
; LENGTH: 379
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-093-463-78

Query Match      78.5%; Score 1174.5; DB 15; Length 379;
Best Local Similarity 78.0%; Pred. No. 4e-108;
Matches 216; Conservative 22; Mismatches 36; Indels 3; Gaps 1;

QY 1 GSHSLRYPSTAVSRPGGEPRYIAVEYVDDTQFLRFDSDAAIPRMEPRPWPVEQGPYW 60
DB 25 GSHSNRYFSAVSRPGGEPRFIAMGYVDDTQFVRFDSDSACPRMEPRAPWVEQGPYW 84
QY 61 EWTGTGAKANAQTRVALNRLNRYNOSEA---GSHTLQMGNGCDMGDPGRLLRGVHOA 117
DB 85 EESTRNTKAAQTRDMNLQTLRGYNQSGVPGSGHTLQWMTGCDLGS DGRLLRGYEQYA 144
QY 118 YDGDYISLNE DLRSWTAADTVAQITQFYBAEYABEFRTYLRGECLELLRRYLENGKE 177
DB 145 YDGRDYALNEDLRSWTAADTAAQISKRKCEANVAEQRRAYLGSTCVEMHLRYLENGKE 204
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QY 178 TLORADPPKAAVAAHPIISDHEATLRCWALGFYPAEITLITWDRGDEQDTQDTLVELVETRPAG 237  
DQ 205 MLQADPPKTHVTHHPVDFYEALRCWALGFYPAEITLITWDRGDEQDTQDTLVELVETRPAG 264  
QY 238 DGTFFQKAAVVPVSGEQRXYCHVQHEGLPQPLILRW 274  
DQ 265 DGTFFQKAAVVPVSGEQRXYCHVQHEGLPEPLMLRW 301

## RESULT 9

US-09-819-371-6  
; Sequence 6, Application US/09819371  
; Publication No. US20040053344A1  
; GENERAL INFORMATION:  
; APPLICANT: Egawa, Kohji  
; TITLE OF INVENTION: Cancer Cell-Specific HLA-F Antigen and a Diagnostic Method of Can  
; FILE REFERENCE: 30815  
; CURRENT APPLICATION NUMBER: US/09/819,371  
; CURRENT FILING DATE: 2002-03-15  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: Patentin version 3.0  
; SEQ ID NO 6  
; LENGTH: 215  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-819-371-6

Query Match 77.8%; Score 1164; DB 12; Length 215;  
Best Local Similarity 99.5%; Pred. No. 2e-107;  
Matches 214; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 23 IAVEYVDDTQFLRFDSDAAIPRMEPEPWPVEQSGPQYWEWTTGYAKANAQTDRAVALRNL 82  
DQ 1 IAVEYVDDTQFLRFDSDAAIPRMEPEPWPVEQSGPQYWEWTTGYAKANAQTDRAVALRNL 60  
QY 83 RRYNQSFAGHTLQGMNGCDMPDGRLLRGYHAYDGDYIISINEDLSWTAADTVAQI 142  
DQ 61 RRYNQSFAGHTLQGMNGCDMPDGRLLRGYHAYDGDYIISINEDLSWTAADTVAQI 120  
QY 143 TQFYAEAEVABFRITVLEGECLLRLRYLNGKETLQADPPKAAVAAHPIISDHEATLR 202  
DQ 121 TQFYAEAEVABFRITVLEGECLLRLRYLNGKETLQADPPKAAVAAHPIISDHEATLR 180  
QY 203 CWALGFYPAEITLITWDRGDEQDTQDTLVELVETRPAG 237  
DQ 181 CWALGFYPAEITLITWDRGDEQDTQDTLVELVETRPAG 215

## RESULT 10

US-10-093-463-80  
; Sequence 80, Application US/10093463  
; Publication No. US20030208039A1  
; GENERAL INFORMATION:  
; APPLICANT: Padigaru, Muralidhara  
; APPLICANT: Shenoy, Suresh  
; APPLICANT: Kekuda, Ramesh  
; APPLICANT: Gusev, Vladimir  
; APPLICANT: Pochart, Pascal  
; APPLICANT: Zhong, Mei  
; APPLICANT: Rastelli, Luca  
; APPLICANT: Mezes, Peter  
; APPLICANT: Smithson, Glenda  
; APPLICANT: Guo, Xiaojia  
; APPLICANT: Gerlach, Valerie  
; APPLICANT: Casman, Stacie  
; APPLICANT: Boldog, Ferenc  
; APPLICANT: Li, Li  
; APPLICANT: Zerkhusen, Bryan  
; APPLICANT: Tchernev, Velizar  
; APPLICANT: Gangolli, Esha  
; APPLICANT: Vernet, Corine  
; APPLICANT: Pena, Carol

; APPLICANT: Burgess, Catherine  
; APPLICANT: Liu, Xiaohong  
; APPLICANT: Spytek, Kimberly  
; APPLICANT: Gorman, Linda  
; APPLICANT: Spaderna, Steven  
; APPLICANT: Voss, Edward  
; APPLICANT: Malyankar, Uriel  
; APPLICANT: Anderson, David  
; APPLICANT: Patturajan, Meera  
; APPLICANT: Miller, Charles  
; APPLICANT: Taupier, Raymond J. Jr.  
; TITLE OF INVENTION: No. US20030208039A1el Antibodies that Bind to Antigenic Polypept  
; FILE REFERENCE: 21402-290A (Cura 590AT)  
; CURRENT APPLICATION NUMBER: US/10/093,463  
; CURRENT FILING DATE: 2002-06-24  
; PRIOR APPLICATION NUMBER: 60/283,675  
; PRIOR FILING DATE: 2001-04-14  
; PRIOR APPLICATION NUMBER: 60/338,092  
; PRIOR FILING DATE: 2001-12-03  
; PRIOR APPLICATION NUMBER: 60/274,281  
; PRIOR FILING DATE: 2001-03-08  
; PRIOR APPLICATION NUMBER: 60/274,101  
; PRIOR FILING DATE: 2001-03-08  
; PRIOR APPLICATION NUMBER: 60/325,681  
; PRIOR FILING DATE: 2001-09-27  
; PRIOR APPLICATION NUMBER: 60/304,354  
; PRIOR FILING DATE: 2001-07-10  
; PRIOR APPLICATION NUMBER: 60/279,995  
; PRIOR FILING DATE: 2001-03-30  
; PRIOR APPLICATION NUMBER: 60/294,899  
; PRIOR FILING DATE: 2001-05-31  
; PRIOR APPLICATION NUMBER: 60/287,424  
; PRIOR FILING DATE: 2001-04-30  
; PRIOR APPLICATION NUMBER: 60/299,027  
; PRIOR FILING DATE: 2001-06-18  
; PRIOR APPLICATION NUMBER: 60/309,198  
; PRIOR FILING DATE: 2001-07-31  
; PRIOR APPLICATION NUMBER: 60/281,194  
; PRIOR FILING DATE: 2001-04-04  
; PRIOR APPLICATION NUMBER: 60/274,194  
; PRIOR FILING DATE: 2001-03-08  
; PRIOR APPLICATION NUMBER: 60/274,849  
; PRIOR FILING DATE: 2001-03-09  
; PRIOR APPLICATION NUMBER: 60/330,380  
; PRIOR FILING DATE: 2001-10-18  
; PRIOR APPLICATION NUMBER: 60/275,235  
; PRIOR FILING DATE: 2001-03-12  
; PRIOR APPLICATION NUMBER: 60/288,342  
; PRIOR FILING DATE: 2001-05-03  
; PRIOR APPLICATION NUMBER: 60/275,578  
; PRIOR FILING DATE: 2001-03-13  
; NUMBER OF SEQ ID NOS: 370  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 80  
; LENGTH: 364  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-093-463-80

Query Match 77.4%; Score 1158; DB 15; Length 364;  
Best Local Similarity 77.4%; Pred. No. 1.7e-106;  
Matches 212; Conservative 25; Mismatches 37; Indels 0; Gaps 0;  
QY 1 GSHSLRYFSTAVSRGEGEPRIYAVYVDQFLRFDSDAAIPRMEPEPWPVEQSGPQY 60  
DQ 25 GSHSLRYFSTAVSRGEGEPRIYAVYVDQFLRFDSDAAIPRMEPEPWPVEQSGLEYW 84  
QY 61 EWTGYSKANAQTDRAVALRNLRLRYNQSEAGSHITQGMNGCDMPDGRLLRGYHAYD 120  
DQ 85 DQETRNAKHAQIYRNLRLRYNQSEAGSHITQGMNGCDMPDGRLLRGYHAYD 144  
QY 121 KDYISINEDLSWTAADTVAQITQFYAEAEVABFRITVLEGECLLRLRYLNGKETLQ 180

Db 145 KDYLALNEDLSHTAANTAAQISQKWEADRYSEQVRAYLEGKCMWLRHLENGKETLQ 204  
Qy 181 RADPPKARVAHPISDHEATLRCWALGFYPAEITLTWQDGEEOQTQDTLVELTRPADGDT 240  
Db 205 HADPPKARVHTQPSIDHEATLRCWALGFYPAEITLTWQDGEDQDTQDTLVELTRPADGDT 264  
Qy 241 FQKWAAVVPSGEGEORYTCHVOHEGLPQPLILRW 274  
Db 265 FQKWAAVVPSGEGEORYTCHVOHEGLPEPLILRW 298

## RESULT 11

US-10-138-888-23  
; Sequence 23, Application US/1013888  
; Publication No. US20030148972A1  
; GENERAL INFORMATION:  
; APPLICANT: Thomas, Winston J.  
; Drayna, Dennis T.  
; Feder, John N.  
; Gnirke, Andreas  
; Ruddy, David  
; Tsuchihashi, Zenta  
; Wolff, Roger K.  
; TITLE OF INVENTION: Hereditary Hemochromatosis Gene  
; NUMBER OF SEQUENCES: 79  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds LLP  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036-2711

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/138,888  
FILING DATE: 02-May-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/834,497  
FILING DATE: 04-APR-1997  
APPLICATION NUMBER: US 08/652,265  
FILING DATE: 23-MAY-1996  
APPLICATION NUMBER: US 08/632,673  
FILING DATE: 16-APR-1996  
APPLICATION NUMBER: US 08/630,912  
FILING DATE: 04-APR-1996

## ATTORNEY/AGENT INFORMATION:

NAME: Brian M. Poissant  
REGISTRATION NUMBER: 28,462  
REFERENCE/DOCKET NUMBER: 8907-095-999  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-8864

## INFORMATION FOR SEQ ID NO: 23:

SEQUENCE CHARACTERISTICS:  
LENGTH: 365 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FEATURE:  
NAME/KEY: Protein  
LOCATION: 1..365  
OTHER INFORMATION: /note= "Human Major Histocompatibility  
Class I (MHC) protein"  
SEQUENCE DESCRIPTION: SEQ ID NO: 23:  
US-10-138-888-23

Query Match 77.1%; Score 1154; DB 14; Length 365;  
Best Local Similarity 77.0%; Pred. No. 4.1e-106;  
Matches 211; Conservative 21; Mismatches 42; Indels 0; Gaps 0;  
Qy 1 GSHSLRYVESTAVSRPGRGEPRIYAVYVDDTQFLRFDSDAAIPRMEPRPWPVEQEGPQYW 60  
Db 25 GSHSMRYFTTSVSRPGRGEPRIYAVYVDDTQFLRFDSDAAISQRMFPRAPWIEQEGPEYW 84  
Qy 61 EWTGTVAKANAQTDRLVALNRLRRYNSQSEAGSHTLQMGNGCDMGPDGRLRLRGYHAYDQ 120  
Db 85 DGETRKKVKAHSQTHRVLDGLTGLRGYNSQSEAGSHTLQMGFGCDVGSDFRGLRGYHAYDQ 144  
Qy 121 KDYISLNEDLSRWTAAQITQRYEAEYEAEBFRTYLEGECLELLRRLYLENGKETLQ 180  
Db 145 KDYIALKEDLSRWTAAQITQRYEAEYEAEBFRTYLEGECLELLRRLYLENGKETLQ 204  
Qy 181 RADPPKARVAHPISDHEATLRCWALGFYPAEITLTWQDGEEOQTQDTLVELTRPADGDT 240  
Db 205 RTDAPKTHMTTHAVSDHEATLRCWALGFYPAEITLTWQDGEDQDTQDTLVELTRPADGDT 264  
Qy 241 FQKWAAVVPSGEGEORYTCHVOHEGLPQPLILRW 274  
Db 265 FQKWAAVVPSGEGEORYTCHVOHEGLPKPLILRW 298

## RESULT 12

US-10-073-300-6  
; Sequence 6, Application US/10073300  
; Publication No. US20030003535A1  
; GENERAL INFORMATION:  
; APPLICANT: Reiter, Yoram  
; TITLE OF INVENTION: SINGLE CHAIN CLASS I MAJOR HISTO- COMPATIBILITY COMPLEXES  
; FILE REFERENCE: 02/23339  
; CURRENT APPLICATION NUMBER: US/10/073,300  
; CURRENT FILING DATE: 2002-06-25  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 6  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-073-300-6

Query Match 77.1%; Score 1153; DB 14; Length 280;  
Best Local Similarity 76.6%; Pred. No. 3.6e-106;  
Matches 210; Conservative 22; Mismatches 42; Indels 0; Gaps 0;

Qy 1 GSHSLRYVESTAVSRPGRGEPRIYAVYVDDTQFLRFDSDAAIPRMEPRPWPVEQEGPQYW 60  
Db 1 GSHSMRYFTTSVSRPGRGEPRIYAVYVDDTQFLRFDSDAAISQRMFPRAPWIEQEGPEYW 60  
Qy 61 EWTGTVAKANAQTDRLVALNRLRRYNSQSEAGSHTLQMGNGCDMGPDGRLRLRGYHAYDQ 120  
Db 61 DGETRKKVKAHSQTHRVLDGLTGLRGYNSQSEAGSHTLQMGFGCDVGSDFRGLRGYHAYDQ 120  
Qy 121 KDYISLNEDLSRWTAAQITQRYEAEYEAEBFRTYLEGECLELLRRLYLENGKETLQ 180  
Db 121 KDYIALKEDLSRWTAAQITQRYEAEYEAEBFRTYLEGECLELLRRLYLENGKETLQ 180  
Qy 181 RADPPKARVAHPISDHEATLRCWALGFYPAEITLTWQDGEEOQTQDTLVELTRPADGDT 240  
Db 181 RTDAPKTHMTTHAVSDHEATLRCWALGFYPAEITLTWQDGEDQDTQDTLVELTRPADGDT 240  
Qy 241 FQKWAAVVPSGEGEORYTCHVOHEGLPQPLILRW 274  
Db 241 FQKWAAVVPSGEGEORYTCHVOHEGLPKPLILRW 274

## RESULT 13

US-10-075-257-6  
; Sequence 6, Application US/10075257  
; Publication No. US20040086960A1  
; GENERAL INFORMATION:

APPLICANT: Reiter, Yoram  
TITLE OF INVENTION: SINGLE CHAIN CLASS I MAJOR HISTO-COMPATIBILITY COMPLEXES,  
FILE REFERENCE: 02/23338  
CURRENT FILING DATE: 2002-06-25  
NUMBER OF SEQ ID NOS: 20  
SOFTWARE: Patent in version 3.2  
SEQ ID NO 6  
LENGTH: 280  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-075-257-6

Query Match 77.1%; Score 1153; DB 16; Length 280;  
Best Local Similarity 76.6%; Pred. No. 6.2e-106;  
Matches 210; Conservative 22; Mismatches 42; Indels 0; Gaps 0;

QY 1 GSHSLRYFSTAVSRPGEGPRYIAVEYDDTQFLRPSDAAIPRMEPRPWEQEGPQYW 60  
DB 1 GSHSMRYFTSVSRPGEGPRFIAGVYDDTQFVRPDSDAASQRMPEPRAPWIEQEGPEYW 60  
QY 61 EWTGCAKANAQTRVALRNLRLRYNQSEAGSHTLQGMNGCDMGPDGRLRLRYLGHQYAYDG 120  
DB 61 DGETRKVKAHSQTHRVLDLGLRGYNNQSEAGSHTVQRMYGCDVGSDFRFLRGYHQAAYDG 120  
QY 121 KQYISLNEDLRSWTAADTVAQITQRFYAEYAEAEFFRYLGECELELLRRLRYLGHQYAYDG 180  
DB 121 KQYIALKEDLRSWTAADMAAQTTHKWEAAHVAEQRLAYLEGTCTVFWLRYLGHQYAYDG 180  
QY 181 RADPPKAHVAHPISDHEATLRCAWALGFYPAEITLTWQDGEQDTDELVETRPAGDGT 240  
DB 181 RTDAPKTHMTHAVSDHEATLRCAWALGFYPAEITLTWQDGEQDTDELVETRPAGDGT 240  
QY 241 FQKWAAVVVPSEGEQRYTCHVQHEGLPQPLILRW 274  
DB 241 FQKWAAVVVPSEGEQRYTCHVQHEGLPQPLILRW 274

RESULT 14  
US-10-073-300-5  
Sequence 5, Application US/10073300  
Publication No. US20030003535A1  
GENERAL INFORMATION:  
APPLICANT: Reiter, Yoram  
TITLE OF INVENTION: SINGLE CHAIN CLASS I MAJOR HISTO- COMPATIBILITY COMPLEXES  
FILE REFERENCE: 02/23339  
CURRENT FILING DATE: 2002-06-25  
NUMBER OF SEQ ID NOS: 20  
SOFTWARE: Patent in version 3.0  
SEQ ID NO 5  
LENGTH: 415  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: human beta2 microglobulin linked to MHC class I heavy chain  
US-10-073-300-5

Query Match 77.1%; Score 1153; DB 14; Length 415;  
Best Local Similarity 76.6%; Pred. No. 6.2e-106;  
Matches 210; Conservative 22; Mismatches 42; Indels 0; Gaps 0;

QY 1 GSHSLRYFSTAVSRPGEGPRYIAVEYDDTQFLRPSDAAIPRMEPRPWEQEGPQYW 60  
DB 116 GSHSMRYFTSVSRPGEGPRFIAGVYDDTQFVRPDSDAASQRMPEPRAPWIEQEGPEYW 175  
QY 61 EWTGCAKANAQTRVALRNLRLRYNQSEAGSHTLQGMNGCDMGPDGRLRLRYLGHQYAYDG 120  
DB 61 DGETRKVKAHSQTHRVLDLGLRGYNNQSEAGSHTVQRMYGCDVGSDFRFLRGYHQAAYDG 120  
QY 121 KQYISLNEDLRSWTAADTVAQITQRFYAEYAEAEFFRYLGECELELLRRLRYLGHQYAYDG 180  
DB 121 KQYIALKEDLRSWTAADMAAQTTHKWEAAHVAEQRLAYLEGTCTVFWLRYLGHQYAYDG 180  
QY 181 RADPPKAHVAHPISDHEATLRCAWALGFYPAEITLTWQDGEQDTDELVETRPAGDGT 240  
DB 181 RTDAPKTHMTHAVSDHEATLRCAWALGFYPAEITLTWQDGEQDTDELVETRPAGDGT 240  
QY 241 FQKWAAVVVPSEGEQRYTCHVQHEGLPQPLILRW 274  
DB 241 FQKWAAVVVPSEGEQRYTCHVQHEGLPQPLILRW 274

Search completed: June 18, 2004, 19:22:13  
Job time : 52 secs

Db 236 KDYIALKEDLRSWTAADMAAQTTHKWEAAHVAEQRLAYLEGTCTVFWLRYLGHQYAYDG 295  
QY 181 RADPPKAHVAHPISDHEATLRCAWALGFYPAEITLTWQDGEQDTDELVETRPAGDGT 240  
DB 296 RTDAPKTHMTHAVSDHEATLRCAWALGFYPAEITLTWQDGEQDTDELVETRPAGDGT 355  
QY 241 FQKWAAVVVPSEGEQRYTCHVQHEGLPQPLILRW 274  
DB 356 FQKWAAVVVPSEGEQRYTCHVQHEGLPQPLILRW 389

RESULT 15  
US-10-075-257-5  
Sequence 5, Application US/10075257  
Publication No. US20040086960A1  
GENERAL INFORMATION:  
APPLICANT: Reiter, Yoram  
TITLE OF INVENTION: SINGLE CHAIN CLASS I MAJOR HISTO-COMPATIBILITY COMPLEXES,  
FILE REFERENCE: 02/23338  
CURRENT FILING DATE: 2002-02-15  
NUMBER OF SEQ ID NOS: 20  
SOFTWARE: Patent in version 3.2  
SEQ ID NO 5  
LENGTH: 415  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Human beta2 microglobulin linked to MHC class I heavy chain  
US-10-075-257-5

Query Match 77.1%; Score 1153; DB 16; Length 415;  
Best Local Similarity 76.6%; Pred. No. 6.2e-106;  
Matches 210; Conservative 22; Mismatches 42; Indels 0; Gaps 0;

QY 1 GSHSLRYFSTAVSRPGEGPRYIAVEYDDTQFLRPSDAAIPRMEPRPWEQEGPQYW 60  
DB 116 GSHSMRYFTSVSRPGEGPRFIAGVYDDTQFVRPDSDAASQRMPEPRAPWIEQEGPEYW 175  
QY 61 EWTGCAKANAQTRVALRNLRLRYNQSEAGSHTLQGMNGCDMGPDGRLRLRYLGHQYAYDG 120  
DB 176 DGETRKVKAHSQTHRVLDLGLRGYNNQSEAGSHTVQRMYGCDVGSDFRFLRGYHQAAYDG 235  
QY 121 KQYISLNEDLRSWTAADTVAQITQRFYAEYAEAEFFRYLGECELELLRRLRYLGHQYAYDG 180  
DB 236 KDYIALKEDLRSWTAADMAAQTTHKWEAAHVAEQRLAYLEGTCTVFWLRYLGHQYAYDG 295  
QY 181 RADPPKAHVAHPISDHEATLRCAWALGFYPAEITLTWQDGEQDTDELVETRPAGDGT 240  
DB 296 RTDAPKTHMTHAVSDHEATLRCAWALGFYPAEITLTWQDGEQDTDELVETRPAGDGT 355  
QY 241 FQKWAAVVVPSEGEQRYTCHVQHEGLPQPLILRW 274  
DB 356 FQKWAAVVVPSEGEQRYTCHVQHEGLPQPLILRW 389

Search completed: June 18, 2004, 19:22:13  
Job time : 52 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 18, 2004, 19:19:06 ; Search time 18 Seconds  
(without alignments)  
792.623 Million cell updates/sec

Title: US-09-819-371-5  
Perfect score: 1496  
Sequence: 1 GSHSLRYSTAVSRPGRGP.....QRYTCHVQHEGLPQLILRW 274

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_42.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1496	100.0	362	1	HLAF_HUMAN
2	1471	98.3	346	1	P30511 homo sapien
3	1416	94.7	348	1	P33617 macaca mula
4	1228	82.9	362	1	P30389 homo sapien
5	1227	82.0	362	1	P30381 gorilla gor
6	1227	82.0	362	1	P30475 homo sapien
7	1227	82.0	362	1	P30436 homo sapien
8	1226	82.0	363	1	P31612 homo sapien
9	1224	81.8	362	1	P30460 homo sapien
10	1224	81.8	362	1	P30480 homo sapien
11	1223	81.8	362	1	P30379 gorilla gor
12	1223	81.8	362	1	P30447 homo sapien
13	1223	81.8	365	1	P18463 homo sapien
14	1222	81.7	362	1	P30380 gorilla gor
15	1221	81.6	362	1	P30389 homo sapien
16	1221	81.6	362	1	P30452 homo sapien
17	1221	81.6	362	1	P30484 homo sapien
18	1221	81.6	366	1	P30508 homo sapien
19	1221	81.6	366	1	P30508 homo sapien
20	1220	81.5	362	1	P30505 homo sapien
21	1219	81.5	366	1	P30505 homo sapien
22	1218	81.4	359	1	P13750 pan troglod
23	1218	81.4	362	1	P30432 homo sapien
24	1217	81.4	362	1	P30433 homo sapien
25	1216	81.3	362	1	P30495 homo sapien
26	1216	81.3	362	1	P31610 homo sapien
27	1216	81.3	365	1	P05534 homo sapien
28	1216	81.3	366	1	P30510 homo sapien
29	1215	81.2	362	1	P13751 pan troglod
30	1215	81.1	362	1	P30385 homo sapien
31	1213	81.1	362	1	P30484 homo sapien
32	1212	81.0	362	1	P16210 pan troglod
33	1212	81.0	362	1	P30498 homo sapien

ALIGNMENTS

RESULT 1

ID	HLAF_HUMAN	STANDARD	PRT	362 AA
AC	P30511			
DT	01-APR-1993 (Rel. 25, Created)			
DT	01-APR-1993 (Rel. 25, Last sequence update)			
DT	28-FEB-2003 (Rel. 41, Last annotation update)			
DE	HLA class I histocompatibility antigen, alpha chain F precursor (HLA F antigen) (leukocyte antigen F) (CD412).			
GN	HLA-F OR HLAF OR HLA-5.4.			
OS	Homo sapiens (Human)			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=90111605; PubMed=1688605;			
RA	Geraghty D.E., Wei X., Orr H.T., Koller B.H.;			
RT	"Human leukocyte antigen F (HLA-F). An expressed HLA gene composed of a class I coding sequence linked to a novel transcribed repetitive element.";			
RL	J. Exp. Med. 171:1-18(1990).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=91197889; PubMed=1707659;			
RA	Lary D., Epstein H., Holmes N.;			
RT	"The human class I MHC gene HLA-F is expressed in lymphocytes.";			
RL	Int. Immunol. 2:531-537(1990).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RA	Shiina S., Taniya G., Oka A., Inoko H.;			
RT	"Homo sapiens 2,229,817bp genomic DNA of 6p21.3 HLA class I region.";			
RL	Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.			
CC	-!- FUNCTION: Involved in the presentation of foreign antigens to the immune system.			
CC	-!- SUBUNIT: Heterodimer of an alpha chain and a beta chain (beta-2-microglobulin).			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).			
CC	EMBL; X17093; CAA34947.1; ..			
DR	EMBL; AF000521; BAB63337.1; ..			
DR	PIR; A60384; A60384.			
DR	HSSP; Q30201; 1A62.			
DR	Genew; HGNC:4963; HLA-F.			
DR	MIM; 143110; ..			
DR	GO; GO:0030106; F:MHC class I receptor activity; TAS.			
DR	InterPro; IPR007110; Ig-like.			
DR	InterPro; IPR003597; Ig_c1.			
DR	InterPro; IPR003006; Ig_MHC.			

34	1210	80.9	365	1	1A01_SAGEO
35	1209	80.8	366	1	1C02_GORGO
36	1209	80.8	366	1	1C04_GORGO
37	1208	80.7	362	1	1B82_HUMAN
38	1207	80.7	362	1	1B48_HUMAN
39	1206	80.6	366	1	1C03_GORGO
40	1206	80.6	366	1	1C03_HUMAN
41	1205	80.5	365	1	1A30_HUMAN
42	1205	80.5	366	1	1C06_HUMAN
43	1203	80.4	362	1	1B35_HUMAN
44	1203	80.4	362	1	1B59_HUMAN
45	1202	80.3	362	1	1B18_HUMAN

P30515	saguinus oe
P30385	gorilla gor
P30387	gorilla gor
Q29718	homo sapien
P30486	homo sapien
P30386	gorilla gor
P04222	homo sapien
P16188	homo sapien
Q29963	homo sapien
P30685	homo sapien
Q29940	homo sapien
P30466	homo sapien

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DR InterPro; IPR001039; MHC_I.
DR Pfam; PF00047; Ig_1.
DR Pfam; PF00129; MHC_I; 1.
DR PRINTS; PR01638; MHCCLASSI.
DR PRODOM; PD000050; MHC_I; 1.
DR SMART; SM00407; IGc1; 1.
DR PROSITE; PS00835; IG LIKE; 1.
DR PROSITE; PS00290; IG MHC; 1.
KW MHC I; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 21
FT CHAIN 22 362
FT DOMAIN 22 111
FT DOMAIN 112 203
FT DOMAIN 204 295
FT DOMAIN 296 305
FT TRANSMEM 306 329
FT DOMAIN 330 362
FT DISULFID 122 185
FT DISULFID 224 280
FT CARBOHYD 107 107
SQ SEQUENCE 362 AA; 40568 MW; B8DD041F820A34E1 CRC64;

Query Match 100.0%; Score 1496; DB 1; Length 362;
Best Local Similarity 100.0%; Pred. No. 4e-113; Indels 0; Gaps 0;
Matches 274; Conservative 0; Mismatches 0;

QY 1 GSHSLRYFSTAVSRPGCEPRYIAVEYVDDTQFLRFDSDAAIPRMEPREPWEQEGPQYW 60
DB 22 GSHSLRYFSTAVSRPGCEPRYIAVEYVDDTQFLRFDSDAAIPRMEPREPWEQEGPQYW 81
QY 61 EWTGYAKANAQTDRAVALNLLRRYNSQSEAGSHTLQGNMGCDMPDGLRLRGYHAYDG 120
DB 82 EWTGYAKANAQTDRAVALNLLRRYNSQSEAGSHTLQGNMGCDMPDGLRLRGYHAYDG 141
QY 121 KDYSISNEDLSRWSAATAADVAQITQRFYAEAYAEFFRYLGECELELLRRYLENGKETLQ 180
DB 142 KDYSISNEDLSRWSAATAADVAQITQRFYAEAYAEFFRYLGECELELLRRYLENGKETLQ 201
QY 181 RADPPKAHVAHPISDHEATRLCWALGFYPAEITLTWQDGEQTDTELVEPTRPADGDT 240
DB 202 RADPPKAHVAHPISDHEATRLCWALGFYPAEITLTWQDGEQTDTELVEPTRPADGDT 261
QY 241 FQKAAVAVVPSGEEQRYTCHVQHEGLPQLILRW 274
DB 262 FQKAAVAVVPSGEEQRYTCHVQHEGLPQLILRW 295

RESULT 3
HLAF MACMU STANDARD; PRT; 348 AA.
ID HLAF MACMU
AC P33617;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
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DE HLA class I histocompatibility antigen, alpha chain F precursor (HLA F  
DE antigen) (leukocyte antigen F).  
GN HLA-F OR HLA-F.  
OS Macaca mulatta (Rhesus macaque).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
OC Cercopithecinae; Macaca.  
OX NCBI\_TaxID=9544;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=93246295; PubMed=8482576;  
RA Otting N., Bontrop R.E.;  
RT "Characterization of the rhesus macaque (Macaca mulatta) equivalent  
RT of HLA-F";  
RL Immunogenetics 38:141-145(1993).  
CC -!- FUNCTION: Involved in the presentation of foreign antigens to the  
CC immune system.  
CC -!- SUBUNIT: Heterodimer of an alpha chain and a beta chain (beta-2-  
CC microglobulin).  
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CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
CC -----  
DR EMBL; Z21819; CAA79885.1; -.  
DR PIR; S29990; S29990.  
DR HSSP; Q30201; 1A6Z.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig cl.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR001039; MHC\_I.  
DR Pfam; PF00047; Ig; 1.  
DR Pfam; PF00129; MHC I; 1.  
DR PRINTS; PR01638; MHCCLASSI.  
DR ProDom; PD000050; MHC I; 1.  
DR SMART; SM00407; IGL1-1.  
DR PROSITE; PS00835; IG\_LIKE; 1.  
DR PROSITE; PS00290; IG\_MHC; 1.  
KW MHC I; Transmembrane; Glycoprotein; Signal.  
FT SIGNAL 1 21  
FT CHAIN 22 348  
FT ALPHA CHAIN F.  
FT DOMAIN 22 113  
FT DOMAIN 114 205  
FT DOMAIN 206 297  
FT DOMAIN 298 307  
FT TRANSMEM 308 331  
FT DOMAIN 332 348  
FT DISULFID 124 187  
FT DISULFID 226 282  
FT CARBOHYD 109 109  
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Query Match 94.7%; Score 1416; DB 1; Length 348;  
Best Local Similarity 94.9%; Pred. No. 1e-106;  
Matches 262; Conservative 4; Mismatches 8; Indels 2; Gaps 1;  
QY 1 GSHSLRYFSTAVSRPGRGP- -RYIAVEYDDTQFLRPSDAAIPMEPRPWEQEGPQ 58  
DB 22 GSHSLRYFSTAVSRPGRGPQRYIAVSYVDDTQFLRPSDAAIPMEPRPWEQEGPQ 81  
QY 59 YWMTTGYAKANACTDRVALNLLRRYNQSEASHTLQNGMCDMGPDGRLRLGYHOHAY 118  
DB 82 YWMTTGYAKANACTDRVALNLLRRYNQSEASHTLQNGMCDMGPDGRLRLGYHOHAY 141  
QY 119 DGKDYISLNDLSWTAADTVAQITQRYEAEYAEFFTYLEGCLELLRRLYLENGKET 178  
DB 142 DGKDYISLNDLSWTAADTVAQITQRYEAEYAEFFTYLEGCLELLRRLYLENGKET 201

QY 179 LQRADPPKAVHHPISDHEATLRCWALGFPAEITLTWQDGEBOQDTELVEITPAGD 238  
DB 202 LQRADPPKAVHHPISDHEATLRCWALGFPAEITLTWQDGEBOQDTELVEITPAGD 261  
QY 239 GTFQKAAVAVVPSGEQRYTCHVQHEGLPQPLILRW 274  
DB 262 GTFQKAAVAVVPSGEQRYTCHVQHEGLPQPLILRW 297  
RESULT 4  
ID 1B27 HUMAN STANDARD; PRT; 362 AA.  
AC P03989; P10317; P10318; P19373; P30467; Q08136; Q29693; Q29846;  
AC Q29861;  
DT 23-OCT-1986 (Rel. 02, Created)  
DT 13-AUG-1987 (Rel. 05, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE HLA class I histocompatibility antigen, B-27 alpha chain precursor  
DE (MHC class I antigen B\*27).  
GN HLA-B OR HLAB.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A. (B\*2701).  
RX MEDLINE=86138405; PubMed=3912316;  
RA Weiss E.H., Kuon W., Doerner C., Lang M., Riethmuller G.;  
RT "Organization, sequence and expression of the HLA-B27 gene: a  
RT molecular approach to analyze HLA and disease associations.";  
RL Immunobiology 170:367-380(1985).  
RN [2]  
RP SEQUENCE OF 25-361 FROM N.A. (B\*2701).  
RX MEDLINE=86149317; PubMed=3485286;  
RA Szoets H., Riethmuller G., Weiss E., Mao T.;  
RT "Complete sequence of HLA-B27 cDNA identified through the  
RT characterization of structural markers unique to the HLA-A, -B, and  
RT -C allelic series.";  
RL Proc. Natl. Acad. Sci. U.S.A. 83:1428-1432(1986).  
RN [3]  
RP SEQUENCE OF 25-295 (B\*2701).  
RX MEDLINE=85226361; PubMed=2408663;  
RA Ezquerria A., Bragado R., Vega M.A., Strominger J.L., Woody J.,  
RA Lopez de Castro J.A.;  
RT "Primary structure of papain-solubilized human histocompatibility  
RT antigen HLA-B27.";  
RL Biochemistry 24:1733-1741(1985).  
RN [4]  
RP SEQUENCE FROM N.A. (B\*2701 AND B\*2702).  
RX MEDLINE=86220133; PubMed=3011411;  
RA Seemann G.H.A., Rein R.S., Brown C.S., Ploegh H.L.;  
RT "Gene conversion-like mechanisms may generate polymorphism in human  
RT class I genes.";  
RL EMBO J. 5:547-552(1986).  
RN [5]  
RP SEQUENCE FROM N.A. (B\*2702).  
RX MEDLINE=96086486; PubMed=7482496;  
RA Moses J.H., Marsh S.G.E., Arnett K.L., Adams E.J., Bodmer J.G.,  
RA Parham P.;  
RT "On the nucleotide sequences of B\*2702 and B\*2705.";  
RL Tissue Antigens 46:50-53(1995).  
RN [6]  
RP SEQUENCE OF 86-107 AND 171-181 (B\*2702).  
RX MEDLINE=86042671; PubMed=2414775;  
RA Vega M.A., Ezquerria A., Rojo S., Aparicio P., Bragado R.,  
RA Lopez de Castro J.A.;  
RT "Structural analysis of an HLA-B27 functional variant: identification  
RT of residues that contribute to the specificity of recognition by  
RT cytolytic T lymphocytes";  
RL Proc. Natl. Acad. Sci. U.S.A. 82:7394-7398(1985).  
RN [7]  
RP SEQUENCE FROM N.A. (B\*2703).  
RX MEDLINE=88227491; PubMed=3286582;  
RP

RA Choo S.Y., St John T., Orr H.T., Hansen J.A.;  
 RT "Molecular analysis of the variant alloantigen HLA-B\*2703 (HLA-B\*2703)  
 RT identifies a unique single amino acid substitution.";  
 RL Hum. Immunol. 21:209-219(1998).  
 RN [8]  
 RP SEQUENCE FROM N.A. (B\*2704 AND B\*2706).  
 RX MEDLINE=96134006; PubMed=8550101.  
 RA Rudwaleit M., Bowness P., Wordsworth P.;  
 RT "The nucleotide sequence of HLA-B\*2704 reveals a new amino acid  
 RT substitution in exon 4 which is also present in HLA-B\*2706.";  
 RL Immunogenetics 43:160-162(1996).  
 RN [9]  
 RP SEQUENCE FROM N.A. (B\*2706).  
 RX MEDLINE=94102824; PubMed=8276469;  
 RA Vilches C., de Pablo R., Kreisler M.;  
 RT "Nucleotide sequence of HLA-B\*2706.";  
 RL Immunogenetics 39:219-219(1994).  
 RN [10]  
 RP SEQUENCE FROM N.A. (B\*2707).  
 RX MEDLINE=91268545; PubMed=1711072;  
 RA Choo Y.S., Fan L.A., Hansen J.A.;  
 RT "A novel HLA-B\*27 allele maps B27 allospecificity to the region around  
 RT position 70 in the alpha 1 domain.";  
 RL J. Immunol. 147:174-180(1991).  
 RN [11]  
 RP SEQUENCE FROM N.A. (B\*2708).  
 RX MEDLINE=95064789; PubMed=7974468;  
 RA Hildebrand W.H., Domene J.D., Shen S.Y., Marsh S.G.E., Bunce M.,  
 RA Guttridge M.G., Darke C., Parham P.;  
 RT "The HLA-B\*708 antigen is encoded by a new subtype of HLA-B\*27  
 RT (B\*2708).";  
 RL Tissue Antigens 44:47-51(1994).  
 RN [12]  
 RP SEQUENCE FROM N.A. (B\*2709).  
 RX MEDLINE=94375872; PubMed=8089488;  
 RA Del Porto P., D'Amato M., Florillo M.T., Tuosto L., Piccolella E.,  
 RA Sorrentino R.;  
 RT "Identification of a novel HLA-B\*27 subtype by restriction analysis of  
 RT a cytotoxic gamma/delta T cell clone.";  
 RL J. Immunol. 153:3093-3100(1994).  
 RN [13]  
 RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 25-300.  
 RX MEDLINE=92405152; PubMed=1525820;  
 RA Madden D.R., Gorga J.C., Strominger J.L., Wiley D.C.;  
 RT "The three-dimensional structure of HLA-B\*27 at 2.1-A resolution  
 RT suggests a general mechanism for tight peptide binding to MHC.";  
 RL Cell 70:1035-1048(1992).  
 RN [14]  
 RP X-RAY CRYSTALLOGRAPHY.  
 RX MEDLINE=92018187; PubMed=1922337;  
 RA Madden D.R., Gorga J.C., Strominger J.L., Wiley D.C.;  
 RT "The structure of HLA-B\*27 reveals nonamer self-peptides bound in an  
 RT extended conformation.";  
 RL Nature 353:321-325(1991).  
 RN [15]  
 RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 25-300.  
 RX MEDLINE=22344622; PubMed=12244049;  
 RA Hulemeyer M., Hillig R.C., Voiz A., Ruhl M., Schroder W., Saenger W.,  
 RA Ziegler A., Uchanska-Ziegler B.;  
 RT "HLA-B\*27 subtypes differentially associated with disease exhibit  
 RT subtle structural alterations.";  
 RL J. Biol. Chem. 277:47844-47853(2002).  
 RN [16]  
 RP 3D-STRUCTURE MODELING OF 115-206.  
 RX MEDLINE=95148615; PubMed=7846047;  
 RA Rognan D., Scapozza L., Folkers G., Daser A.;  
 RT "Rational design of nonnatural peptides as high-affinity ligands for  
 RT the HLA-B\*2705 human leukocyte antigen.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 92:753-757(1995).  
 CC -!- FUNCTION: Involved in the presentation of foreign antigens to the  
 CC immune system.  
 CC -!- SUBUNIT: Heterodimer of an alpha chain and a beta chain (beta-2-

CC microglobulin).  
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -!- POLYMORPHISM: The following alleles of B-27 are known:  
 CC B\*2701-B\*2705, B\*2702 (B27.2; B-27K; B27e), B\*2703 (B27d), B\*2704,  
 CC B\*2706, B\*2707, B\*2708 (B7Qui) and B\*2709 (B27-ci). The sequence  
 CC shown is that of B\*2701.  
 CC -!- DISBASE: HLA-B27 is associated with the development of ankylosing  
 CC spondylitis.  
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 CC -----  
 CC DR EMBL; X03945; CAA27578.1; ALT\_SEQ.  
 CC DR EMBL; X03664; CAA27301.1; -.  
 CC DR EMBL; X03667; CAA27301.1; JOINED.  
 CC DR EMBL; L38504; AAG69724.1; -.  
 CC DR EMBL; M54883; AAG59616.1; -.  
 CC DR EMBL; X03685; CAA27302.1; -.  
 CC DR EMBL; X03686; CAA27302.1; JOINED.  
 CC DR EMBL; M12967; AAG36221.1; -.  
 CC DR EMBL; U27608; AAC50444.1; -.  
 CC DR EMBL; U35734; AAC50447.1; -.  
 CC DR EMBL; X73578; CAA51980.1; -.  
 CC DR EMBL; M62852; AAG59647.1; -.  
 CC DR EMBL; L19923; AAG59658.1; -.  
 CC DR EMBL; Z33453; CAA83876.1; -.  
 CC DR PIR; I37515; I37515.  
 CC DR PIR; I56116; I56116.  
 CC DR PIR; S07441; HLUH2.  
 CC DR PDB; 1HSA; 15-OCT-92.  
 CC DR PDB; 1ROG; 30-SEP-94.  
 CC DR PDB; 1ROH; 30-SEP-94.  
 CC DR PDB; 1ROI; 30-SEP-94.  
 CC DR PDB; 1ROJ; 30-SEP-94.  
 CC DR PDB; 1ROK; 30-SEP-94.  
 CC DR PDB; 1ROL; 30-SEP-94.  
 CC DR PDB; 1JGE; 23-DEC-02.  
 CC DR Genew; HGNC:4932; HLA-B.  
 CC DR MIM; 142830; -.  
 CC DR InterPro; IPR007110; Ig-like.  
 CC DR InterPro; IPR003597; Ig\_C1.  
 CC DR InterPro; IPR003006; Ig\_MHC.  
 CC DR InterPro; IPR001039; MHC\_I.  
 CC DR Pfam; PF00047; Ig; 1.  
 CC DR Pfam; PF00129; MHC\_I; 1.  
 CC DR PRINTS; PR01638; MHCCLASSI.  
 CC DR ProDom; PD000050; MHC\_I; 1.  
 CC DR SMART; SMC0407; IgC1; 1.  
 CC DR PROSITE; PS00835; IG\_LIKE; 1.  
 CC DR PROSITE; PS00290; IG\_MHC; 1.  
 CC DR MHC I; Transmembrane; Glycoprotein; Signal; Polymorphism;  
 CC 3D-structure. 1 24  
 CC SIGNAL 25 362 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,  
 CC CHAIN B-27 ALPHA CHAIN.  
 CC FT DOMAIN 25 114 EXTRACELLULAR ALPHA-1.  
 CC FT DOMAIN 115 206 EXTRACELLULAR ALPHA-2.  
 CC FT DOMAIN 207 298 EXTRACELLULAR ALPHA-3.  
 CC FT DOMAIN 299 308 CONNECTING PEPTIDE.  
 CC FT TRANSMEM 309 332  
 CC  
 CC Query Match 82.9%; Score 1240; DB 1; Length 362;  
 CC Best Local Similarity 82.8%; Pred. No. 1.5e-92;  
 CC Matches 227; Conservative 14; Mismatches 33; Indels 0; Gaps 0;  
 CC  
 CC QY 1 GSHSLVFEFATVSRPGRGPRVIAYVVDVDTQFLRFDSDAATPRMEPRPFWVEQGFQYW 60  
 CC DB 25 GSHSMRYFTHSVSRPGRGPRFITVGVVDVDTLFRFDSDAASPRFPAPFWIEQGFQYW 84



RP SEQUENCE FROM N.A. (B\*3909).  
RC TISSUE=Blood;  
RX MEDLINE=96435466; PubMed=8838352;  
RA Ramos M., Postigo J.M., Vilches C., Layrisse Z., Lopez de Castro J.A.;  
RT "Primary structure of a novel HLA-B\*39 allele (B\*3909) from the Warao  
RL Indians of Venezuela. Further evidence for local HLA-B diversification  
RT in South America.";  
RL Tissue Antigens 46:401-404(1995).  
[5]  
RP SEQUENCE FROM N.A. (B\*3906).  
RX Zhao W., Fernandez-Vina M.A., Lazaro A.M., Araujo H.A., Miller S.,  
RA Stastny P.;  
RT "Full cDNA of a novel HLA-B\*39 subtype, B\*39061.";  
RL Tissue Antigens 47:435-437(1996).  
[6]  
RP SEQUENCE FROM N.A. (B\*3906).  
RX Zhang L., Ellexson M.E., Hildebrand W.H.;  
RA Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.  
[7]  
RP SEQUENCE FROM N.A. (B\*3910).  
RX MEDLINE=97142356; PubMed=8989545;  
RA Wells R.S., Parham P.;  
RT "A novel recombinant HLA-B\*39 allele (B\*3910) in a South African  
RL Zulu.";  
RL Tissue Antigens 48:595-597(1996).  
[8]  
RP SEQUENCE FROM N.A. (B\*3901).  
RX MEDLINE=97378891; PubMed=9234488;  
RA Vilches C., Bunce M., de Pablo R., Moreno M.E., Puente S., Sanz L.,  
RA Kreisler M.;  
RT "The novel HLA-Cw\*1802 allele is associated with B\*5703 in the Bubi  
RL population from Equatorial Guinea.";  
RL Tissue Antigens 49:644-648(1997).  
[9]  
RP SEQUENCE FROM N.A. (B\*3901).  
RX Kashiwase K.;  
RA Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.  
[10]  
RP SEQUENCE FROM N.A. (B\*3924).  
RC TISSUE=Peripheral blood;  
RX MEDLINE=22447027; PubMed=12559815;  
RA Estefania E., Gomez-Lozano N., de Pablo R., Moreno M.E., Vilches C.;  
RT "Complementary DNA sequence of the HLA-B\*3924 allele.";  
RL Eur. J. Immunogenet. 30:11-12(2003).  
[11]  
RP SEQUENCE OF 10-362 FROM N.A. (B\*3908).  
RX MEDLINE=96435470; PubMed=8838356;  
RA Adams B.J., Little A.-M., Arnett K.L., McAuley J.E., Williams R.C.,  
RA Parham P.;  
RT "Three new HLA-B alleles found in Mexican-Americans.";  
RL Tissue Antigens 46:414-416(1995).  
[12]  
RP SEQUENCE OF 26-206 FROM N.A. (B\*3912).  
RX MEDLINE=99299758; PubMed=10372543;  
RA Marcos C.Y., Fernandez-Vina M.A., Lazaro A.M., Moraes M.E.,  
RA Moraes J.R., Stastny P.;  
RT "Novel HLA-A and HLA-B alleles in South American Indians.";  
RL Tissue Antigens 53:476-485(1999).  
[13]  
RP SEQUENCE OF 26-206 FROM N.A. (B\*3912).  
RX MEDLINE=20066996; PubMed=10600013;  
RA Lazaro A.M., Moraes M.E., Marcos C.Y., Moraes J.R.,  
RA Fernandez-Vina M.A., Stastny P.;  
RT "Evolution of HLA-class I compared to HLA-class II polymorphism in  
RL Terena, a South-American Indian tribe.";  
RL Hum. Immunol. 60:1138-1149(1999).  
[14]  
RP SEQUENCE OF 26-206 FROM N.A. (B\*3923).  
RX MEDLINE=21160452; PubMed=11260515;  
RA Akesaka T., Kashiwase K., Ishikawa Y., Tanaka H., Shimizu M.,  
RA Kawai S., Akaza T., Takahashi T., Juji T.;  
RT "Allele frequency of HLA-B\*39 in the Japanese population and

RT identification of a novel B39 allele, B\*3923.";  
RL Tissue Antigens 57:169-172(2001).  
[15]  
RP SEQUENCE OF 60-196 FROM N.A. (B\*3907).  
RX MEDLINE=95317819; PubMed=7797264;  
RA Garber T.L., Butler L.M., Trachtenberg E.A., Erlich H.A., Rickards O.,  
RA De Stefano G., Watkins D.I.;  
RT "HLA-B alleles of the Cayapa of Ecuador: new B39 and B15 alleles.";  
RL Immunogenetics 42:19-27(1995).  
CC -!- FUNCTION: Involved in the presentation of foreign antigens to the  
CC immune system.  
CC -!- SUBUNIT: Heterodimer of an alpha chain and a beta chain (beta-2-  
CC microglobulin).  
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -!- POLYMORPHISM: The following alleles of B-39 are known: B\*3901  
CC (B\*39.1), B\*3902 (B\*2), B\*3903, B\*3904 (B39N), B\*3905 (ST-16),  
CC B\*3906 (B39G), B\*3907 (B39uw3), B\*3909, B\*3910, B\*3912 (B3901v),  
CC B\*3923 (B39022v1) and B\*3924. The sequence shown is that of  
CC B\*3901.  
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CC  
CC  
CC EMBL; M94052; AAA52658.1; -  
CC EMBL; M94051; AAA52660.1; -  
CC EMBL; M94053; AAA52659.1; -  
CC EMBL; U04243; AAA87396.1; -  
CC EMBL; L36318; AAA73942.1; -  
CC EMBL; L22649; AAA69861.1; -  
CC EMBL; U29480; AAC50392.1; -  
CC EMBL; L42024; AAB59484.1; -  
CC EMBL; U29083; AAC32741.1; -  
CC EMBL; U56246; AAB01985.1; -  
CC EMBL; Y09058; CAA70261.1; -  
CC EMBL; AB091216; BAC11810.1; -  
CC EMBL; AB091218; BAC11811.1; -  
CC EMBL; A5428252; AAN63555.1; -  
CC EMBL; L42280; AAB51452.1; -  
CC EMBL; U76395; AAB39108.1; -  
CC EMBL; U76394; AAB39108.1; JOINED.  
CC EMBL; AB032097; BAA84116.1; -  
CC EMBL; U15640; AAA74047.1; -  
CC PIR; I38876; I38876.  
CC PIR; I54314; I54314.  
CC PIR; I54505; I54505.  
CC PIR; I68850; I68850.  
CC PIR; I84488; I84488.  
CC HSSP; P30460; IAGD.  
CC Genew; HGNC:4932; HLA-B.  
CC MIM; 142830; -  
CC GO; GO:0005887; C:integral to plasma membrane; NAS.  
CC GO; GO:0030106; F:MHC class I receptor activity; NAS.  
CC GO; GO:0006955; P:immune response; NAS.  
CC InterPro; IPR007110; IG-like.  
CC InterPro; IPR003597; IG-cl.  
CC InterPro; IPR003006; IG\_MHC.  
CC InterPro; IPR001039; MHC\_I.  
CC Pfam; PF00047; ig; 1.  
CC Pfam; PF00129; MHC\_I; 1.  
CC PRINTS; PR01638; MHCCLASSI.  
CC ProDom; PD000050; MHC\_I; 1.  
CC SMART; SM00407; IGcl; 1.  
CC PROSITE; PS00835; IG\_LIKE; 1.  
CC PROSITE; PS00290; IG\_MHC; 1.  
CC MHC I; Transmembrane Glycoprotein; Signal; Polymorphism.  
CC SIGNAL 1 24  
CC CHAIN 25 362 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,  
CC B-39 ALPHA CHAIN.  
CC FT  
CC FT

```
FT DOMAIN 25 114 EXTRACELLULAR ALPHA-1.
FT DOMAIN 115 206 EXTRACELLULAR ALPHA-2.
FT DOMAIN 207 298 EXTRACELLULAR ALPHA-3.
FT DOMAIN 299 308 CONNECTING PEPTIDE.
FT TRANSMEM 309 332
FT DOMAIN 333 362 CYTOPLASMIC TAIL.
FT CARBOHYD 110 110 N-LINKED (GLCNAC. .) (BY SIMILARITY).
FT DISULFID 125 188 BY SIMILARITY.
FT DISULFID 227 293 BY SIMILARITY.
FT VARIANT 33 33 Y-->D (in allele B*3912).
FT VARIANT 35 35 /FTID=VAR_016659.
FT VARIANT 35 35 S-->A (in allele B*3904 and allele
FT B*3912).
FT /FTID=VAR_016421.

Query Match 82.0%; Score 1227; DB 1; Length 362;
Best Local Similarity 81.8%; Pred. No. 1.7e-91;
Matches 224; Conservative 18; Mismatches 32; Indels 0; Gaps 0;

QY 1 GSHSLRYFSTAVSRGPGRPYIAVYDDTQPLRFDSDAALPRMEPRFPWVEQGPQYW 60
DB 25 GSHSMEYFYTSVRGPGRPYISGVYDDTQVRFDSDAASPRFPAPWIEQGPETW 84
QY 61 EWTGTGAKANAQDRVALNRLRRYNSQSGSHTLQNGGCDGPPGRLRLGYHQHAYDG 120
DB 85 DNTQTCIKTNTQTDRESLRNLGYYNQSGSHTLQRMVYCDVPGDRLRGHNPAYDG 144
QY 121 KDVISNELRLSTAAATVAQITQRYEAEAEPTVLEGBCLLRLRYLNGKXETLQ 180
DB 145 KDVIALLNEDLSSWTAADTAQITQRYEAEAEPTVLEGBCLLRLRYLNGKXETLQ 204
QY 181 RADPPKXAHVHPISDHEATLRCWALGFYPAETITLWQDGEQTOCTELVETRPAGDGT 240
DB 205 RADPPKXTHVHPISDHEATLRCWALGFYPAETITLWQDGEQTOCTELVETRPAGDRT 264
QY 241 FOKAAVVPVSGEQRVYCHVQEGPPOPILRW 274
DB 265 FOKAAVVPVSGEQRVYCHVQEGPPOPILRW 298

RESULT 7
1B67 HUMAN STANDARD; PRT; 362 AA.
AC Q29836; Q29678; Q8NC5; Q951A6; Q9BD38;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE HLA class I histocompatibility antigen, B-67 alpha chain precursor
DE (MHC class I antigen B*67).
DE HLA-B OR HLAB.
GN Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (B*6701).
RX MEDLINE=34294981; Pubmed=7517584;
RA Little A.-M., Domene J.D., Hildebrand W.H., Shen S.Y., Barber L.D.,
RA Marsh S.G.E., Bias W.B., Parham P.;
RT "HLA-B*67: a member of the HLA-B*67 family that expresses the ME1
RT epitope.";
RL Tissue Antigens 43:38-43 (1994).
RN [2]
RP SEQUENCE OF 26-205 FROM N.A. (B*6701).
RC TISSUE=Blood;
RA Peterdorff E.;
RT "Molecular diversity of HLA-B*67";
RL Submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A. (B*6702).
RA Iglehart B.A., Leffell M.S.;
RT "HLA-B*6702 (Promoter-3'UTR).";
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
```

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[4]
RN SEQUENCE OF 26-206 FROM N.A. (B*6702).
RP Balasare L.A., Hurley C.K.;
RT "Novel HLA-B allele (HLA-B*67012 variant)";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Involved in the presentation of foreign antigens to the
CC immune system.
CC -!- SUBUNIT: Heterodimer of an alpha chain and a beta chain (beta-2-
CC microglobulin).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- POLYMORPHISM: The following alleles of B-67 are known: B*6701
CC (B-67LAV) and B*6702. The sequence shown is that of B*6701.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; L17005; AAC37548.1; -
DR EMBL; U18789; AAB60360.1; -
DR EMBL; AF487379; AAL93257.1; -
DR EMBL; AF321835; AAK09378.1; -
DR EMBL; AF321834; AAK09378.1; JOINED.
DR EMBL; AY050196; AAL18235.1; -
DR EMBL; AY050195; AAL18235.1; JOINED.
DR PIR; I59645; I59645.
DR HSSP; P30460; 1AGD.
DR Gensu; HGNC:4932; HLA-B.
DR MIM; 142830; -
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR001039; MHC_I.
DR Pfam; PF00047; Ig; 1.
DR PRINTS; PF00129; MHC_I; 1.
DR PRINTS; PR01638; MHCCLASSI.
DR ProDom; PD000050; MHC_I; 1.
DR SMART; SM00407; IGcl; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
DR PROSITE; PS00290; IG_MHC; 1.
KW MHC I; Transmembrane; Glycoprotein; Signal; Polymorphism.
FT SIGNAL 1 24
FT CHAIN 25 362 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
FT B-67 ALPHA CHAIN.
FT DOMAIN 25 114 EXTRACELLULAR ALPHA-1.
FT DOMAIN 115 206 EXTRACELLULAR ALPHA-2.
FT DOMAIN 207 298 EXTRACELLULAR ALPHA-3.
FT DOMAIN 299 308 CONNECTING PEPTIDE.
FT TRANSMEM 309 332
FT DOMAIN 333 362 CYTOPLASMIC TAIL.
FT CARBOHYD 110 110 N-LINKED (GLCNAC. .) (BY SIMILARITY).
FT DISULFID 125 188 BY SIMILARITY.
FT DISULFID 227 283 E-->G (in allele B*6702).
FT VARIANT 69 69 /FTID=VAR_016536.
FT VARIANT 76 76 I-->V (in allele B*6702).
FT VARIANT 87 87 N-->E (in allele B*6702).
FT VARIANT 90 90 /FTID=VAR_016537.
FT VARIANT 93 93 I-->K (in allele B*6702).
FT VARIANT 97 97 A-->R (in allele B*6702).
FT VARIANT 100 100 T-->A (in allele B*6702).
FT VARIANT 100 100 /FTID=VAR_016541.
FT VARIANT 100 100 E-->V (in allele B*6702).
FT SEQUENCE 362 AA; 40342 MW; 3F6A17FC10230F70 CRC64;
SQ SEQUENCE 82.0%; Score 1227; DB 1; Length 362;
Query Match
```

RESULT 8

1873 HUMAN STANDARD; PRT; 363 AA.

ID 1873 HUMAN

AC Q31612;

CD 10-OCT-2003 (Rel. 42, Created)

DT 10-OCT-2003 (Rel. 42, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE HLA class I histocompatibility antigen, B\*73 alpha chain precursor

DE (MHC class I antigen B\*73).

DE HLA-B OR HLAB.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OX NCBI\_TaxID:9606;

RN [1]

RP SEQUENCE FROM N.A. (B\*7301).

RP MEDLINE=95026796; PubMed=7524186;

RA Farham P., Arnett K.L., Adams E.J., Barber L.D., Domena J.D.,

RA Stewart D., Haldebrand W.H., Little A.-M.;

RT "The HLA-B\*73 antigen has a most unusual structure that defines a

RT second lineage of HLA-B alleles.;"

RL Tissue Antigens 43:302-313(1994).

RN [2]

RP SEQUENCE FROM N.A. (B\*7301).

RP MEDLINE=94299292; PubMed=7517915;

RA Vilches C., de Pablo R., Herrero M.J., Moreno M.E., Kreisler M.;

RT "HLA-B\*73: an atypical HLA-B molecule carrying a Bw6-epitope motif

RT variant and a B pocket identical to HLA-B27.;"

RL Immunogenetics 40:166-166(1994).

RN [3]

RP SEQUENCE FROM N.A. (B\*7301).

RP MEDLINE=96164742; PubMed=8547229;

RA Hoffmann H.J., Kristensen T.J., Jensen T.G., Graugaard B., Lamm L.U.;

RT "Antigenic characteristics and cDNA sequences of HLA-B\*73.;"

RL Eur. J. Immunogenet. 22:231-240(1995).

RN [4]

RP SEQUENCE FROM N.A. (B\*7301).

RP TISSUE=Blood;

RC MEDLINE=22512041; PubMed=12622774;

RA Cox S.T., McWhinnie A.J., Robinson J., Marsh S.G.E., Farham P.,

RA Madrigal J.A., Little A.-M.;

RT "Cloning and sequencing full-length HLA-B and -C genes.;"

RL Tissue Antigens 61:20-48(2003)

CC -1- FUNCTION: Involved in the presentation of foreign antigens to the

CC immune system.

CC -1- SUBUNIT: Heterodimer of an alpha chain and a beta chain (beta-2-

CC microglobulin).

CC -1- SUBCELLULAR LOCATION: Type I membrane protein.

CC -----

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CC EMBL; U04787; AAA53175.1; -;  
 CC EMBL; X77658; CAA54739.1; -;  
 CC EMBL; L24373; AAA96723.1; -;  
 CC EMBL; AJ311601; CAC35319.1; -;  
 CC PIR; I37512; S42102.  
 CC HSSP; P03989; 1HSA.  
 CC Genew; HGNC:4932; HLA-B.  
 CC MIM; 142830; -;  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003597; Ig\_c1.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR001039; MHC\_I.  
 DR Pfam; PF00047; ig; 1.  
 DR Pfam; PF00129; MHC\_I; 1.  
 DR PRINTS; PR01638; MHCCLASSI.  
 DR ProDom; PD000050; MHC\_I; 1.  
 DR SMART; SM00407; Igc1; 1.  
 DR ProSITE; PS50835; IG\_LIKE; 1.  
 DR ProSITE; PS00290; IG\_MHC; 1.  
 KW MHC I; transmembrane; Glycoprotein; Signal.  
 FT SIGNAL 1 24  
 FT CHAIN 25 363

HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,  
 B-73 ALPHA CHAIN.  
 DOMAIN 25 114  
 DOMAIN 115 206  
 DOMAIN 207 298  
 DOMAIN 299 308  
 TRANSMEM 309 323  
 DOMAIN 334 363  
 FT CARBOHYD 110 110  
 FT DISULFID 125 188  
 FT DISULFID 227 283  
 SQ SEQUENCE 363 AA; 40435 MW; 04522E97C1E11C40 CRC64;

CYTOPLASMIC TAIL.  
 N-LINKED (GLCNAC. . .) (BY SIMILARITY).  
 BY SIMILARITY.  
 BY SIMILARITY.

Query Match 82.0%; Score 1226; DB 1; Length 363;  
 Best Local Similarity 81.84; Pred.No.2e-91;  
 Matches 224; Conservative 16; Mismatches 34; Indels 0; Gaps 0;

Qy 1 GSHSLRYFSTAVSRGRGEPRIYAEVDDTQTLRFDSDAAI PRMEPRFPWFQEGPQYW 60  
 Db 25 GSHSMRYFHTSVSRGGEPRFITGVYDDTQTVRFDSDAASPREEPRAFWEQGEPEYW 84  
 Qy 61 EWTGTGAKAQAQDTRVALRNLLRRYNOSEAGSHTLQMGNGMDGPDGELLARGVHCHAYDG 120  
 Db 85 DRNTQICKAQAQDTRVGLRNLRGYNQSEDSGSHTWQTMYGCDMGPDGRLLRGYNQFAYDG 144  
 Qy 121 KDVI SLNEDLRSWTAADTVAQITQRFYEABEYAEFEPTYLEGECLLELLRYLENGKETLQ 180  
 Db 145 KDVI ALNEDLRSWTAADTAQITQKWEARVAEQRLAYLEGECEVWLRRLHLENGKETLQ 204  
 Qy 181 RADPPKAFVAHPHISDHEATLRCAWLGFPYPAETITLTWQRGEBOQTQDTLVEITPAGDGT 240  
 Db 205 RADPEKTHVTHHFI SDHEATLRCAWLGFPYPAETITLTWQRGDDQTDQDTLVEITPAGDGT 264  
 Qy 241 FQKWAAYVPSGGEQRYTCHVQHEGLPQPLIRW 274  
 Db 265 FQKWAAYVPSGGEQRYTCHVQHEGLQEPCTLRW 298

RESULT 9  
 1B08 HUWAN  
 ID 1B08 HUWAN STANDARD; PRU: 362 AA.  
 AC P030460; Q62901; Q95730; Q98140; P79542; Q95369; Q95J00; Q9GJ20;  
 AC Q9MY78; Q9MYF4; Q9TQH6; Q9TQMG; Q9UQT0;  
 DT 01-APR-1993 (Rel. 25, Created)



DT 01-APR-1993 (Rel. 25, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE HLA class I histocompatibility antigen, B-8 alpha chain precursor  
 DE (MHC class I antigen B\*8).  
 GN HLA-B OR HLAB.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A. (B\*0801).  
 RX MEDLINE=89235215; PubMed=2715640;  
 RA Parham P., Lawlor D.A., Lomen C.E., Ennis P.D.;  
 RT "Diversity and diversification of HLA-A,B,C alleles."  
 RL J. Immunol. 142:3937-3950(1989).  
 RN [2]  
 RP SEQUENCE FROM N.A. (B\*0801).  
 RX TISSUE=Blood;  
 RA Madrigal J.A., Little A.-M.;  
 RT "Cloning and sequencing full-length HLA-B and -C genes."  
 RL Tissue Antigens 61:20-48(2003).  
 RN [3]  
 RP SEQUENCE FROM N.A. (B\*0801).  
 RA Shiina S., Tamiya G., Oka A., Inoko H.;  
 RT "Homo sapiens 2,229,817bp genomic DNA of 6p21.3 HLA class I region."  
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP SEQUENCE OF 26-206 FROM N.A. (B\*0804).  
 RX MEDLINE=97473039; PubMed=9331954;  
 RA Hoyer R.J., Bratlie A., Schreuder G.M., Hurley C.K.;  
 RT "Characterization of a novel HLA-B allele, B\*0804, in a Norwegian family."  
 RL Tissue Antigens 50:308-310(1997).  
 RN [5]  
 RP SEQUENCE OF 33-257 FROM N.A. (B\*0804).  
 RA Eberle M., Lorentzen D., Iwanaga K.K., Watkins D.I.;  
 RT "Identification of a new HLA-B\*08 variant, B\*08NEW."  
 RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.  
 RN [6]  
 RP SEQUENCE OF 26-206 FROM N.A. (B\*0806).  
 RA Marcos C.Y., Lazaro A.M., Noreen H., Stastny P.;  
 RT "New HLA-B locus allele."  
 RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.  
 RN [7]  
 RP SEQUENCE OF 26-206 FROM N.A. (B\*0807 AND B\*0809).  
 RX MEDLINE=20236861; PubMed=1077103;  
 RA Kennedy C.T., Dodd R., Le T., Wallace R., Ng G., Greville W.D.,  
 RA Kennedy A., Taverniti A., Moses J.H., Clow N., Watson N.,  
 RA Dunkley H.;  
 RT "Routine HLA-B genotyping with PCR-sequence-specific oligonucleotides (PCR-SSO) detects eight new alleles: B\*0807, B\*0809, B\*1551, B\*3529, B\*3532, B\*4025, B\*5304 and B\*5508."  
 RL Tissue Antigens 55:266-270(2000).  
 RN [8]  
 RP SEQUENCE OF 116-206 FROM N.A. (B\*0809).  
 RX MEDLINE=20166355; PubMed=10703615;  
 RA Elsner H.A., Blaszyk R.;  
 RT "Identification of the novel allele HLA-B\*0809 in a Caucasian individual: estimation of allelic potential between B\*08 variants."  
 RL Tissue Antigens 55:74-77(2000).  
 RN [9]  
 RP SEQUENCE OF 26-206 FROM N.A. (B\*0809; B\*0812; B\*0813 AND B\*0814).  
 RX MEDLINE=21276061; PubMed=11380931;  
 RA Steiner N.K., Gans C.P., Kosman C., Baldassarre L.A., Edson S.,  
 RA Jones P.P., Rizzuto G., Pimthanotai N., Koester R., Milton W., Ng J.,  
 RA Hartman R.J., Hurley C.K.;  
 RT "Novel HLA-B alleles associated with antigens in the 8C CREG."  
 RL Tissue Antigens 57:373-375(2001).  
 RN [10]  
 RP SEQUENCE OF 26-206 FROM N.A. (B\*0810).

RA Day S.;  
 RT "A new B\*08 variant allele."  
 RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.  
 RN [11]  
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 25-300.  
 RX MEDLINE=97130420; PubMed=8976183;  
 RA Reid S.W., McAdam S., Smith K.J., Klennerman P., O'Callaghan C.A.,  
 RA Harlos K., Jakobsen B.K., McMichael A.J., Bell J.I., Stuart D.I.,  
 RA Jones E.Y.;  
 RT "Antagonist HIV-1 Gag peptides induce structural changes in HLA B8."  
 RL J. Exp. Med. 184:2279-2286(1996).  
 CC -!- FUNCTION: Involved in the presentation of foreign antigens to the immune system.  
 CC -!- SUBUNIT: Heterodimer of an alpha chain and a beta chain (beta-2-microglobulin).  
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -!- POLYMORPHISM: The following alleles of B-8 are known: B\*0801, B\*0804, B\*0806, B\*0807 (B\*NV), B\*0809 (B\*HM; B\*08HO), B\*0810, B\*0812, B\*0813 and B\*0814. The sequence shown is B\*0801.  
 CC  
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 CC  
 CC EMBL; M24036; AAA52662.1; -  
 DR EMBL; AJ295294; CAC18876.1; -  
 DR EMBL; AP000507; BAB63309.1; -  
 DR EMBL; U67331; AAB07726.1; -  
 DR EMBL; U67330; AAB07726.1; JOINED.  
 DR EMBL; U74386; AAB41720.1; -  
 DR EMBL; AF056484; AAC14124.1; -  
 DR EMBL; AF056483; AAC14124.1; JOINED.  
 DR EMBL; AF105226; AAD05244.1; -  
 DR EMBL; AF127248; AAD31431.1; -  
 DR EMBL; AF127247; AAD31431.1; JOINED.  
 DR EMBL; AJ131853; CAA10522.1; -  
 DR EMBL; AF102560; AAD28165.1; -  
 DR EMBL; AF102559; AAD28165.1; JOINED.  
 DR EMBL; AF226151; AAF36681.1; -  
 DR EMBL; AF226150; AAF36681.1; JOINED.  
 DR EMBL; AF279675; AAF81604.1; -  
 DR EMBL; AF279674; AAF81604.1; JOINED.  
 DR EMBL; AF310145; AAG27470.1; -  
 DR EMBL; AF310144; AAG27470.1; JOINED.  
 DR EMBL; AY016212; AAK38401.1; -  
 DR EMBL; AY016211; AAK38401.1; JOINED.  
 DR EMBL; AJ133101; CAB38945.1; -  
 DR EMBL; AJ133102; CAB38945.1; JOINED.  
 DR PIR; I84431; I84431.  
 DR PDB; IAGB; 16-JUN-97.  
 DR PDB; IAGC; 16-JUN-97.  
 DR PDB; IAGD; 16-JUN-97.  
 DR PDB; IAGE; 16-JUN-97.  
 DR PDB; IAGF; 16-JUN-97.  
 DR PDB; IWI5; 04-FEB-03.  
 DR Genew; HGNC:4932; HLA-B.  
 DR MIM; 142830; -  
 DR GO; GO:0005887; C:integral to plasma membrane; NAS.  
 DR GO; GO:0030106; P:MHC class I receptor activity; NAS.  
 DR GO; GO:0006955; P:immune response; NAS.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003597; IG-cl.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR InterPro; IPR001039; MHC\_I.  
 DR Pfam; PF00047; IG; 1.  
 DR Pfam; PF00129; MHC\_I; 1.  
 DR PRINTS; PR01638; MHC\_I; 1.  
 DR ProDom; PD000050; MHC\_I; 1.  
 DR SMART; SM00407; IGcl\_1.



```
FT SIGNAL 1 24
FT CHAIN 25 362
FT HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
FT B*42 ALPHA CHAIN.
FT DOMAIN 25 114
FT DOMAIN 115 206
FT DOMAIN 207 298
FT DOMAIN 299 303
FT TRANSMEM 310 333
FT DOMAIN 334 362
FT CARBOHYD 110 110
FT DISULFID 125 188
FT DISULFID 227 283
FT VARIANT 33 33
FT Y -> H (in allele B*4202).
FT /FTIG=VAR 016460.
FT SEQUENCE 362 AA; 40333 MW; C9155AB015DEA1BE CRC64;

Query Match 81.8%; Score 1224; DB 1; Length 362;
Best Local Similarity 81.4%; Pred. No. 2.9e-91;
Matches 223; Conservative 21; Mismatches 30; Indels 0; Gaps 0;

QY 1 GSHSLRYFTAVSRPGRGPRYIAVEYVDDTQFLRDSDAALPRMEPRPWEQGGPOYW 60
DB 25 GSHSRNRYFTSVSRPGRGPRISVGVYDDTQFVDFSDAASPREPRAPWIEQGPYEW 84
QY 61 EWTGTGAKANAQTDRLVALNRLRRYNSQSEAGSHTLQGMNGCDMGDPGRLRLRGYHQAIDG 120
DB 85 DRNTQIYKAAQTDRESLNLGRYNSQSEAGSHTLQSMYGCVDGPDGRLRLRGHQAIDG 144
QY 121 KDYISLNEDLSRWTAADTVAQITQRYEAEYAEAEFFTYLEGECELELLRRYLENGKETLQ 180
DB 145 KDYIALNEDLSRWTAADTVAQITQRYEAEYAEAEFFTYLEGECELELLRRYLENGKETLQ 204
QY 181 RADPPKHAHHPISDHEATLRCWALGFYPABITLTWQDGEQTDTELVEPTRPAGDGT 240
DB 205 RADPPKTHVTHHPISDHEATLRCWALGFYPABITLTWQDGEQTDTELVEPTRPAGDRT 264
QY 241 FOKWAAVVPSEGEQRYTCHVQHEGLPQPLILRW 274
DB 265 FOKWAAVVPSEGEQRYTCHVQHEGLPQPLILRW 298

RESULT 11
1B01 GORGO
ID 1B01 GORGO STANDARD; PRT; 362 AA.
AC P30379;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 01-APR-1993 (Rel. 25, Last annotation update)
DE Class I histocompatibility antigen, GOGO-B0101 alpha chain precursor.
OS Gorilla gorilla gorilla (lowland gorilla).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
OX NCBI_TaxID=9595;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92078650; PubMed=1744581;
RA Lawlor D.A., Warren E., Taylor P., Parham P.;
RT "Gorilla class I major histocompatibility complex alleles: comparison to human and chimpanzee class I.";
RL J. Exp. Med. 174:1491-1509(1991).
CC -I- FUNCTION: Involved in the presentation of foreign antigens to the immune system.
CC -I- SUBUNIT: Heterodimer of an alpha chain and a beta chain (beta-2-microglobulin).
CC -----
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CC -----
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EMBL; X60255; CAA42807.1; -.
PIR: JH0539; JH0539.
HSP: P03989; JHSA.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR001039; MHC_I.
DR Pfam; PF00047; Ig; 1.
DR Pfam; PF00129; MHC_I; 1.
DR PRINTS; PR01638; MHCCLASSI.
DR PRODOM; PD000050; MHC_I; 1.
DR SMART; SMO0407; IGCI; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
DR PROSITE; PS00290; IG_MHC; 1.
DR MHC I; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 24
FT CHAIN 25 362
FT CLASS I HISTOCOMPATIBILITY ANTIGEN,
FT GOGO-B0101 ALPHA CHAIN.
FT EXTRACELLULAR ALPHA-1.
FT EXTRACELLULAR ALPHA-2.
FT EXTRACELLULAR ALPHA-3.
FT CONNECTING PEPTIDE.
FT CYTOPLASMIC TAIL.
FT BY SIMILARITY.
FT BY SIMILARITY.
FT BY SIMILARITY.
FT N-LINKED (GLCNAC. .) (BY SIMILARITY).
FT CARBOHYD 110 110
FT SEQUENCE 362 AA; 40170 MW; 419EE29817165A4 CRC64;

Query Match 81.8%; Score 1223; DB 1; Length 362;
Best Local Similarity 81.8%; Pred. No. 3.5e-91;
Matches 224; Conservative 17; Mismatches 33; Indels 0; Gaps 0;

QY 1 GSHSLRYFTAVSRPGRGPRYIAVEYVDDTQFLRDSDAALPRMEPRPWEQGGPOYW 60
DB 25 GSHSRNRYFTSVSRPGRGPRITVGVYDDTQFVDFSDAASPREPRAPWIEQGPYEW 84
QY 61 EWTGTGAKANAQTDRLVALNRLRRYNSQSEAGSHTLQGMNGCDMGDPGRLRLRGYHQAIDG 120
DB 85 DRETQTSKAAQTDRENLRLRYNSQSEAGSHTLQGMNGCDMGDPGRLRLRGYHQAIDG 144
QY 121 KDYISLNEDLSRWTAADTVAQITQRYEAEYAEAEFFTYLEGECELELLRRYLENGKETLQ 180
DB 145 KDYIALNEDLSRWTAADTVAQITQRYEAEYAEAEFFTYLEGECELELLRRYLENGKETLQ 204
QY 181 RADPPKHAHHPISDHEATLRCWALGFYPABITLTWQDGEQTDTELVEPTRPAGDGT 240
DB 205 RADPPKTHVTHHPISDHEATLRCWALGFYPABITLTWQDGEQTDTELVEPTRPAGDGT 264
QY 241 FOKWAAVVPSEGEQRYTCHVQHEGLPQPLILRW 274
DB 265 FOKWAAVVPSEGEQRYTCHVQHEGLPQPLILRW 298

RESULT 12
1B47 HUMAN
ID 1B47 HUMAN STANDARD; PRT; 362 AA.
AC P30485; O19555; O77933; Q95392; Q9GIL3;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE HLA class I histocompatibility antigen, B-47 alpha chain precursor
DE (MHC class I antigen B*47) (Bw-47).
GN HLA-B OR HLAB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (B*4701).
RX MEDLINE=88152906; PubMed=3257938;
RA Zemour J., Ennis P.D., Parham P., Dupont B.;
RT "Comparison of the structure of HLA-Bw47 to HLA-B13 and its
```



SEQUENCE OF 26-206 FROM N.A. (A\*2304 AND A\*2305).  
MEDLINE=21068830; PubMed=11169246;  
Steiner N.K., Edson S.M., Mitten W., Ng J., Hartzman R.J.,  
Hurley C.K.; HLA-A alleles carry previously observed polymorphisms.;  
Seven novel HLA-A alleles carry previously observed polymorphisms.;  
Tissue Antigens 56:551-552(2000).  
-!- FUNCTION: Involved in the presentation of foreign antigens to  
the immune system.  
-!- SUBUNIT: Heterodimer of an alpha chain and a beta chain (beta-2-  
microglobulin).  
-!- SUBCELLULAR LOCATION: Type I membrane protein.  
-!- POLYMORPHISM: The following alleles of A-23 are known: A\*2301,  
A\*2302, A\*2303, A\*2304 and A\*2305. The sequence shown is that of  
A\*2301.  
-----  
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or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
-----  
EMBL; M64742; AAA03662.1; -  
EMBL; AF137080; AAD33736.1; -  
EMBL; AF137079; AAD33736.1; JOINED.  
EMBL; AF102572; AAD28171.1; -  
EMBL; AF102571; AAD28171.1; JOINED.  
EMBL; AF135549; AAD22272.1; -  
EMBL; AF135548; AAD22272.1; JOINED.  
EMBL; AF140860; AAD31878.1; -  
EMBL; AF140859; AAD31878.1; JOINED.  
HSSP; Q95352; IHMK.  
Genew; HGNC:4931; HLA-A.  
MIM; 142800; -  
InterPro; IPR007110; IG-like.  
InterPro; IPR003597; IG\_c1.  
InterPro; IPR003006; IG\_MHC.  
InterPro; IPR001039; MHC\_I.  
Pfam; PF0047; IG; 1.  
Pfam; PF0129; MHC\_I; 1.  
PRINTS; PR01638; MHCCLASS1.  
ProDom; PD000050; MHC\_I; 1.  
SMART; SM00407; IGL1; 1.  
PROSITE; PS50835; IG-LIKE; 1.  
PROSITE; PS00290; IG\_MHC; 1.  
MHC\_I; Transmembrane; Glycoprotein; Signal; Polymorphism.  
KW MHC\_I; Transmembrane; Glycoprotein; Signal; Polymorphism.  
FT SIGNAL 1 24  
FT CHAIN 25 365  
FT HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,  
A-23 ALPHA CHAIN.  
FT DOMAIN 25 114  
FT EXTRACELLULAR ALPHA-1.  
FT DOMAIN 115 206  
FT EXTRACELLULAR ALPHA-2.  
FT DOMAIN 207 298  
FT EXTRACELLULAR ALPHA-3.  
FT TRANSMEM 309 332  
FT CONNECTING PEPTIDE.  
FT CYTOPLASMIC TAIL.  
FT N-LINKED (GLCNAC. .) (BY SIMILARITY).  
FT BY SIMILARITY.  
FT Y -> C (in allele A\*2305).  
FT /FTID=VAR 016606.  
FT K -> N (in allele A\*2303).  
FT /FTID=VAR 016607.  
FT L -> W (in allele A\*2302).  
FT /FTID=VAR 016608.  
FT DG -> EW (in allele A\*2304).  
FT /FTID=VAR 016609.  
FT VARIANT 31 31  
FT VARIANT 151 151  
FT K -> N (in allele A\*2303).  
FT VARIANT 180 180  
FT VARIANT 190 191  
FT VARIANT 365 AA; 40732 MW; C372DE503BF393D0 CRC64;  
SQ SEQUENCE 365 AA; 40732 MW; C372DE503BF393D0 CRC64;  
Query Match 81.8%; Score 1223; DB 1; Length 365;  
Best Local Similarity 81.4%; Pred. No. 3 6e-91;  
Matches 223; Conservative 32; Indels 0; Gaps 0;

QY 1 GSHSLAYFTAVSRPGRGEPRTYAVYVDDTQFLRFDSDAAIPRMEPRPFWVQEGPOYW 60  
DB 25 GSHSMRYFTSVSRPGRGEPRTYAVYVDDTQFLRFDSDAAIPRMEPRPFWVQEGPOYW 84  
QY 61 EWTGTYAKANAQDRVALRNLLRYNQSEAGSHTLQMGNGCDMGDPGRLRLRYGQYHAYDG 120  
DB 85 DEETGKVAHSQDRENLRLRYNQSEAGSHTLQMGNGCDMGDPGRLRLRYGQYHAYDG 144  
QY 121 KDYISLNEJRSWTAADTVAQITQRFYAEYAEFFTYLEGSCLELLRRLYNGKETLQ 180  
DB 145 KDYIALKEDLRSWTAADTVAQITQRFYAEYAEFFTYLEGSCLELLRRLYNGKETLQ 204  
QY 181 RADPPKAVAHPLSDHEATLRCWALGFYPAETTLTWQRDGEQOTQDELVEYTRPADGDT 240  
DB 205 RTDPPKTHMTTHPLSDHEATLRCWALGFYPAETTLTWQRDGEQOTQDELVEYTRPADGDT 264  
QY 241 FQKWAADVVSFGEEQRYTCHVQHEGLPKPLTLRW 274  
DB 265 FQKWAADVVSFGEEQRYTCHVQHEGLPKPLTLRW 298  
RESULT 14  
1B37 HUMAN  
ID 1B37 HUMAN STANDARD; PRT; 362 AA.  
AC P18453; O19627; Q95HA3; Q95HA8; Q95HM9; Q9GJ31;  
DT 01-NOV-1990 (Rel. 15, Created)  
DT 01-NOV-1990 (Rel. 16, Last sequence update)  
DE 10-OCT-2003 (Rel. 42, Last annotation update)  
DE HLA class I histocompatibility antigen, B-37 alpha chain precursor  
DE (MHC class I antigen B\*37).  
GN HLA-B OR HLAB.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
[1]  
RP SEQUENCE FROM N.A. (B\*3701).  
RX MEDLINE=90207291; PubMed=2320591;  
RA Ennis P.D., Zemmour J., Salter R.D., Parham P.;  
RT "Rapid cloning of HLA-A,B CDNA by using the polymerase chain  
reaction: frequency and nature of errors produced in amplification.";  
Proc. Natl. Acad. Sci. U.S.A. 87:2833-2837(1990).  
[2]  
RP SEQUENCE FROM N.A. (B\*3704).  
RX TISSUE=Peripheral blood;  
RX MEDLINE=22025782; PubMed=12028544;  
RA Estefania E., Gomez-Lozano N., de Pablo R., Moreno M.E., Vilches C.;  
RT "Complementary DNA sequence of the novel HLA-B\*3704 allele.";  
Tissue Antigens 59:142-144(2002).  
[3]  
RP SEQUENCE FROM N.A. (B\*3705).  
RX MEDLINE=22131942; PubMed=12135437;  
RA Pyo C.-W., Han H., Kim T.G.;  
RT "Identification of a new HLA-B allele, B\*3705 containing a Bw6  
sequence motif.";  
Tissue Antigens 59:335-337(2002).  
[4]  
RP SEQUENCE OF 1-322 FROM N.A. (B\*3701).  
RA Hurley C.K., Bei M., Rodriguez S., Johnson A.;  
RL Submitted (JUN-1994) to the EMBL/GenBank/DBJ databases.  
[5]  
RP SEQUENCE OF 26-206 FROM N.A. (B\*3704).  
RA Gans C.P., Hurley C.K.;  
RT "Novel HLA-B allele.";  
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.  
CC -!- FUNCTION: Involved in the presentation of foreign antigens to the  
immune system.  
CC -!- SUBUNIT: Heterodimer of an alpha chain and a beta chain (beta-2-  
microglobulin).  
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -!- POLYMORPHISM: The following alleles of B-37 are known: B\*3701,  
B\*3704 and B\*3705. The sequence shown is that of B\*3701.  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

CC -----  
CC ENBL; M32320; AAA36233.1; --  
CC ENBL; AF389378; AAL26224.1; --  
CC ENBL; AF418978; AAL07502.1; --  
CC ENBL; AF284828; AAK82990.1; --  
CC ENBL; AF284826; AAK82990.1; JOINED.  
CC ENBL; AF284827; AAK82990.1; JOINED.  
CC ENBL; U11267; AAA19927.1; --  
CC ENBL; AF303102; AAG21400.1; --  
CC ENBL; AF303101; AAG21400.1; JOINED.  
CC PIR; C35997; C35997.  
CC HSP; P03989; IHSA.  
CC Genew; HGNC:4932; HLA-B.  
CC MIM; 142830; --  
CC InterPro; IPR007110; Ig-like.  
CC InterPro; IPR003597; Ig cl.  
CC InterPro; IPR003006; Ig\_MHC.  
CC InterPro; IPR001039; MHC\_I.  
CC Pfam; PF00047; Ig; 1.  
CC Pfam; PF00129; MHC\_I; 1.  
CC PRINTS; PR01638; MHCCLASSI.  
CC ProDom; PD000050; MHC\_I; 1.  
CC SMART; SM00407; IGcl; 1.  
CC PROSITE; PS00835; IG\_LIKE; 1.  
CC PROSITE; PS00290; IG\_MHC; 1.  
CC MHC I; Transmembrane; Glycoprotein; Signal; Polymorphism.  
CC SIGNAL 1 24  
CC CHAIN 25 362  
CC B-37 ALPHA CHAIN.  
CC HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,  
CC B-37 ALPHA CHAIN.  
CC DOMAIN 25 114  
CC DOMAIN 115 206  
CC DOMAIN 207 298  
CC DOMAIN 299 308  
CC TRANSMEM 309 332  
CC DOMAIN 333 362  
CC CARBOHYD 110 110  
CC DISULFID 125 188  
CC DISULFID 227 283  
CC VARIANT 104 104  
CC VARIANT 106 107  
CC VARIANT 195 195  
CC VARIANT 195 195  
CC /FTID=VAR\_016408.  
CC /FTID=VAR\_016409.  
CC Y -> H (in allele B\*3704).  
CC /FTID=VAR\_016410.  
CC /FTID=VAR\_016410.  
CC FAB4375P05474725 CRC64;  
CC SEQUENCE 362 AA; 40456 MW; 19; Mismatches 32; Indels 0; Gaps 0;  
Query Match 81.7%; Score 1222; DB 1; Length 362;  
Best Local Similarity 81.4%; Pred. No. 4.3e-91;  
Matches 223; Conservative 19; Mismatches 32; Indels 0; Gaps 0;

Qy 1 GSHSLRFPSTAVSRGEGEPRYIAVEYVDDTQFLRFDSDAAIPRMEPEPWVEGPGQYW 60  
Db 25 GSHSMRYFHTSVSRGEGEPRFISGVYVDDTQFLRFDSDAAIPRMEPEPWVEGPGQYW 84  
Qy 61 EWTGYAKANQTDRTVALNRLRYNQSEAGSHYLOQMNGCDMGPDGRLRLGYHQHAYDG 120  
Db 85 DRETQISKNTQTYREDLRTLLRYNQSEAGSHYLOQMNGCDMGPDGRLRLGYHQHAYDG 144  
Qy 121 KDYSLSNEDLRSTAAQDTVAQITQFYAEYAEFPYTYLEGCELELLRRLYNGKETLQ 180  
Db 145 KDYLALNEDLSSTAAQDTVAQITQFYAEYAEFPYTYLEGCELELLRRLYNGKETLQ 204  
Qy 181 RADPKKVAHHPISDHEATLRCWALGFYPAEITLTWQDGEOTQDTLVEVTRPADGDT 240  
Db 205 RADPKKTHVTHPISDHEATLRCWALGFYPAEITLTWQDGEOTQDTLVEVTRPADGDT 264

Qy 241 FQKWAAVVPSEGEQRYTCHVQHEGLPQLILRW 274  
Db 265 FQKWAAVVPSEGEQRYTCHVQHEGLPQLILRW 298

## RESULT 15

ID 1B02 GORGO STANDARD; PRT; 362 AA.  
AC P30380;  
DT 01-APR-1993 (Rel. 25, Created)  
DT 01-APR-1993 (Rel. 25, Last sequence update)  
DT 01-APR-1993 (Rel. 25, Last annotation update)  
DE Class I histocompatibility antigen, GOGO-B0102 alpha chain precursor.  
OS Gorilla gorilla gorilla (lowland gorilla).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.  
OX NCBI\_TaxID=9595;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=92078860; PubMed=1744581;  
RA Lawlor D.A., Warren E., Taylor P., Farham P.;  
RT "Gorilla class I major histocompatibility complex alleles: comparison  
RT to human and chimpanzee class I.";  
RL J. Exp. Med. 174:1491-1509(1991).  
CC -!- FUNCTION: Involved in the presentation of foreign antigens to the  
CC immune system.  
CC -!- SUBUNIT: Heterodimer of an alpha chain and a beta chain (beta-2-  
CC microglobulin).  
CC -----

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CC -----  
CC ENBL; X60693; CAA43101.1; --  
CC PIR; JH0540; JH0540.  
CC HSP; P03989; IHSA.  
CC InterPro; IPR007110; Ig-like.  
CC InterPro; IPR003597; Ig cl.  
CC InterPro; IPR003006; Ig\_MHC.  
CC InterPro; IPR001039; MHC\_I.  
CC Pfam; PF00047; Ig; 1.  
CC Pfam; PF00129; MHC\_I; 1.  
CC PRINTS; PR01638; MHCCLASSI.  
CC ProDom; PD000050; MHC\_I; 1.  
CC SMART; SM00407; IGcl; 1.  
CC PROSITE; PS00835; IG\_LIKE; 1.  
CC PROSITE; PS00290; IG\_MHC; 1.  
CC MHC I; Transmembrane; Glycoprotein; Signal.  
CC SIGNAL 1 24  
CC CHAIN 25 362

CC CLASS I HISTOCOMPATIBILITY ANTIGEN,  
CC GOGO-B0102 ALPHA CHAIN.  
CC EXTRACELLULAR ALPHA-1.  
CC EXTRACELLULAR ALPHA-2.  
CC EXTRACELLULAR ALPHA-3.  
CC CONNECTING PEPTIDE.  
CC CYTOPLASMIC TAIL.  
CC BY SIMILARITY.  
CC BY SIMILARITY.  
CC N-LINKED (GLCNAC. .) (BY SIMILARITY).  
CC SEQUENCE 362 AA; 40204 MW; E19EER2B7CC7BECD CRC64;

Query Match 81.6%; Score 1221; DB 1; Length 362;  
Best Local Similarity 81.8%; Pred. No. 5.1e-91;  
Matches 224; Conservative 16; Mismatches 34; Indels 0; Gaps 0;

Qy 1 GSHSLRFPSTAVSRGEGEPRYIAVEYVDDTQFLRFDSDAAIPRMEPEPWVEGPGQYW 60  
Db 25 GSHSMRYFHTSVSRGEGEPRFISGVYVDDTQFLRFDSDAAIPRMEPEPWVEGPGQYW 84

Qy	61	BWTTGYAKAQTDRVALRNLRLRYNOSAGSHTLQGMNGCDMPDGRLLRGYHQHAYDG	120
Db	85	DRETQTSKAQAQTDRENRIRALRYNOSAGSHTFQRMFGCDVGPDCGRLLRGYSQSAYDG	144
Qy	121	KDYISLNEDELSWTAADTVAQITQRYEAEYAEFEFTYLEGECLELLRRYLENGKETLQ	180
Db	145	KDYIALNEDELSWTAADTAAQITQKWEAAREAEQLRAYLEGTCEWLRRYLENGRETQ	204
Qy	181	RADPEKAHVAHHPISDHEATLRCWALGFYPAEITLTWORGEEOTQDTLVETRPAGDGT	240
Db	205	RADTFKTHVTHHPISDHEATLRCWALGFYPAEITLTWORGEDQIQDTLVETRPAGDGT	264
Qy	241	FKWAAVVVPSGEBQRYTCHVQHEGLPOPLIRW	274
Db	265	FKWAAVVVPSGEBERYTCHVQHEGLPKPLIRW	298

Search completed: June 18, 2004, 19:25:59  
Job time : 19 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 18, 2004, 19:22:16 ; Search time 45 Seconds  
(without alignments)  
1921.155 Million cell updates/sec

Title: US-09-819-371-5

Perfect score: 1496

Sequence: 1 GSHSLRFVSTAVSRGRGP.....ORYTCHVQHEGLPQLILRW 274

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 25:\*\*

- 1: sp\_archaea:\*\*
- 2: sp\_bacteria:\*\*
- 3: sp\_fungi:\*\*
- 4: sp\_human:\*\*
- 5: sp\_invertebrate:\*\*
- 6: sp\_mammal:\*\*
- 7: sp\_mhc:\*\*
- 8: sp\_organelle:\*\*
- 9: sp\_phage:\*\*
- 10: sp\_plant:\*\*
- 11: sp\_rodent:\*\*
- 12: sp\_virus:\*\*
- 13: sp\_vertebrate:\*\*
- 14: sp\_unclassified:\*\*
- 15: sp\_virus:\*\*
- 16: sp\_bacteriap:\*\*
- 17: sp\_archaeap:\*\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1496	100.0	324	7 Q861F0	Q861F0 homo sapien
2	1496	100.0	324	7 Q861E9	Q861E9 homo sapien
3	1496	100.0	346	7 Q8WLP5	Q8WLP5 homo sapien
4	1496	100.0	442	7 Q9SHC0	Q9SHC0 homo sapien
5	1491	99.7	346	7 Q8MGQ1	Q8MGQ1 homo sapien
6	1491	99.7	362	7 Q9TP68	Q9TP68 homo sapien
7	1477	98.7	346	7 Q95IT2	Q95IT2 pan troglod
8	1477	98.7	362	6 Q7YR27	Q7YR27 pan troglod
9	1240	82.9	274	7 Q19692	Q19692 homo sapien
10	1240	82.9	362	7 P79612	P79612 homo sapien
11	1240	82.9	362	7 Q78189	Q78189 homo sapien
12	1239	82.8	362	4 Q29705	Q29705 homo sapien
13	1237	82.7	354	7 Q9MW41	Q9MW41 macaca mula
14	1237	82.7	362	7 Q9MXK1	Q9MXK1 pan troglod
15	1236	82.6	359	7 Q29934	Q29934 homo sapien
16	1235	82.6	362	7 Q9MXI2	Q9MXI2 pan troglod

17	1234	82.5	273	7 Q8SNC9	Q8SNC9 homo sapien
18	1234	82.5	341	7 Q19589	Q19589 homo sapien
19	1234	82.5	362	7 Q9MXD1	Q9MXD1 pan troglod
20	1233	82.4	362	7 Q860I7	Q860I7 homo sapien
21	1232	82.4	298	7 Q9GJF1	Q9GJF1 homo sapien
22	1232	82.4	362	7 Q9TPW6	Q9TPW6 homo sapien
23	1232	82.4	362	7 Q7YQ80	Q7YQ80 homo sapien
24	1230	82.2	363	7 Q8MEG3	Q8MEG3 pan troglod
25	1228	82.1	354	7 Q95530	Q95530 pan troglod
26	1228	82.1	362	7 Q9MXI0	Q9MXI0 pan troglod
27	1228	82.1	362	7 Q9MXL8	Q9MXL8 pan troglod
28	1227	82.0	359	7 Q30711	Q30711 macaca mula
29	1227	82.0	363	7 Q30988	Q30988 pan troglod
30	1225	81.9	365	7 Q9TQ74	Q9TQ74 homo sapien
31	1224	81.8	347	7 Q9MWK1	Q9MWK1 gorilla gor
32	1224	81.8	350	7 Q19691	Q19691 homo sapien
33	1224	81.8	362	7 Q9MXK5	Q9MXK5 pan troglod
34	1224	81.8	362	7 Q9MXM2	Q9MXM2 pan troglod
35	1224	81.8	362	7 Q9TFL5	Q9TFL5 pan troglod
36	1223	81.8	347	7 Q9MWK2	Q9MWK2 gorilla gor
37	1223	81.8	354	7 Q95412	Q95412 hylobates 1
38	1223	81.8	359	7 Q860F2	Q860F2 macaca neme
39	1223	81.8	362	7 Q29637	Q29637 homo sapien
40	1223	81.8	362	7 Q7YQ88	Q7YQ88 homo sapien
41	1222	81.7	361	7 Q9GJ77	Q9GJ77 macaca mula
42	1222	81.7	362	7 Q9MXK4	Q9MXK4 pan troglod
43	1222	81.7	362	7 Q30716	Q30716 macaca mula
44	1222	81.7	362	7 Q9GIX2	Q9GIX2 homo sapien
45	1222	81.7	362	7 Q31602	Q31602 homo sapien

#### ALIGNMENTS

RESULT 1

Q861F0	PRELIMINARY;	PRT;	324 AA.
ID	Q861F0		
AC	Q861F0;		
DT	01-JUN-2003 (TrEMBLrel. 24, Created)		
DT	01-JUN-2003 (TrEMBLrel. 24, Last sequence update)		
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)		
DE	Nonclassical MHC class I antigen (Fragment).		
GN	HLA-F.		
OS	Homo sapiens (Human)		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A. Xu L., Liu Y., Zeng Y.;		
RA	He X., Xu L., Liu Y., Zeng Y.;		
RT	"Nonclassical MHC class I HLA-F.";		
RL	Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AY216682; AAC37689.1; -		
DR	GO; GO:0016020; C-membrane; IEA.		
DR	GO; GO:0006955; P-immune response; IEA.		
DR	InterPro; IPR001064; Crystallin.		
DR	InterPro; IPR007110; IG-like.		
DR	InterPro; IPR003597; IG-cl.		
DR	InterPro; IPR003006; IG_MHC.		
DR	Pfam; PF00047; IG; 1.		
DR	Pfam; PF00129; MHC_I; 1.		
DR	PRINTS; PR01638; MHCCLASSI.		
DR	ProDom; PD000050; MHC_I; 1.		
DR	SMART; SM00407; IGcl; 1.		
DR	PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; 1.		
DR	PROSITE; PS50835; IG_LIKE; 1.		
DR	PROSITE; PS00290; IG_MHC; 1.		
FT	NON_TER	1	
FT	NON_TER	324	324
SQ	SEQUENCE	324 AA;	36518 MW; E3E028177D2716F4 CRC64;

Query Match 100.0%; Score 1496; DB 7; Length 324;



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Best Local Similarity 100.0%; Pred. No. 2.6e-122;
Matches 274; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSHSLRSTAVSRPGGEPRIYAVEYDDTQFLRFDSDAAIPRMEPRPWPVEQGPQYW 60
DB 18 GSHSLRSTAVSRPGGEPRIYAVEYDDTQFLRFDSDAAIPRMEPRPWPVEQGPQYW 77
QY 61 EWTITGAKANAQTDRLVALNLLRRYNQSEAGSHTLQMGNGCDMPDGRLLRGYHQHAYDG 120
DB 78 EWTITGAKANAQTDRLVALNLLRRYNQSEAGSHTLQMGNGCDMPDGRLLRGYHQHAYDG 137
QY 121 KQYISLNEDLSRSTAADTVAQITQRFYEAEEYAEFFTYLEGECELLRRYLENGKETLQ 180
DB 138 KQYISLNEDLSRSTAADTVAQITQRFYEAEEYAEFFTYLEGECELLRRYLENGKETLQ 197
QY 181 RADPPKAAHVAHPISDHEATLRCWALGFYPAEITLTWQDGEEOQTDTLVEVTRPAGDGT 240
DB 198 RADPPKAAHVAHPISDHEATLRCWALGFYPAEITLTWQDGEEOQTDTLVEVTRPAGDGT 257
QY 241 FQKWAAVVPSGEEQRYTCHVQHEGLPQPLILRW 274
DB 258 FQKWAAVVPSGEEQRYTCHVQHEGLPQPLILRW 291

RESULT 2
Q8WLP5 PRELIMINARY; PRT; 324 AA.
AC Q8WLP5;
DT 01-JUN-2003 (TREMELrel. 24, Created)
DT 01-JUN-2003 (TREMELrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE MHC class I antigen (Fragment).
GN HLA-F.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Liu Y., Xu L., Zeng Y., He X.;
RT "A new polymorphism in non-classical MHC class I HLA-F.";
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR001064; Crystallin.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig MHC.
DR InterPro; IPR001039; MHC_I.
DR Pfam; PF00047; Ig; 1.
DR Pfam; PF00129; MHC_I; 1.
DR PRINTS; PR01638; MHCCLASSI.
DR PRODOM; PD000050; MHC_I; 1.
DR SMART; SM00407; Igel; 1.
DR PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; 1.
DR PROSITE; PS00835; IG LIKE; 1.
DR PROSITE; PS00290; IG_MHC; 1.
FT NON_TER 1
FT NON_TER 324
SQ SEQUENCE 324 AA; 36518 MW; E3E028177D271674 CRC64;

Query Match 100.0%; Score 1496; DB 7; Length 324;
Best Local Similarity 100.0%; Pred. No. 2.6e-122;
Matches 274; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSHSLRSTAVSRPGGEPRIYAVEYDDTQFLRFDSDAAIPRMEPRPWPVEQGPQYW 60
DB 18 GSHSLRSTAVSRPGGEPRIYAVEYDDTQFLRFDSDAAIPRMEPRPWPVEQGPQYW 77
QY 61 EWTITGAKANAQTDRLVALNLLRRYNQSEAGSHTLQMGNGCDMPDGRLLRGYHQHAYDG 120
DB 78 EWTITGAKANAQTDRLVALNLLRRYNQSEAGSHTLQMGNGCDMPDGRLLRGYHQHAYDG 137

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QY 121 KQYISLNEDLSRSTAADTVAQITQRFYEAEEYAEFFTYLEGECELLRRYLENGKETLQ 180
DB 138 KQYISLNEDLSRSTAADTVAQITQRFYEAEEYAEFFTYLEGECELLRRYLENGKETLQ 197
QY 181 RADPPKAAHVAHPISDHEATLRCWALGFYPAEITLTWQDGEEOQTDTLVEVTRPAGDGT 240
DB 198 RADPPKAAHVAHPISDHEATLRCWALGFYPAEITLTWQDGEEOQTDTLVEVTRPAGDGT 257
QY 241 FQKWAAVVPSGEEQRYTCHVQHEGLPQPLILRW 274
DB 258 FQKWAAVVPSGEEQRYTCHVQHEGLPQPLILRW 291

RESULT 3
Q8WLP5 PRELIMINARY; PRT; 346 AA.
AC Q8WLP5;
DT 01-WAR-2002 (TREMELrel. 20, Created)
DT 01-WAR-2002 (TREMELrel. 20, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE MHC class Ib antigen.
GN HLA-F.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Ishitani A., Miki A., Williams L.M., Moore Y., Geraghty D.E.;
RT "HLA-E, F, and G polymorphism: genomic sequence defines new variation spanning the nonclassical class I genes.";
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA He X., Liu Y., Xu L., Zeng Y.;
RT "Cloning of full-length HLA-F*0101 variant 1 cDNA from Han Chinese.";
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA He X., Xu L., Liu Y., Zeng Y.;
RT "Cloning of full-length HLA-F*0101 variant 2 cDNA from Han Chinese.";
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF523285; AAM74980.1; -
DR EMBL; AF523286; AAM74981.1; -
DR EMBL; AF523287; AAM74982.1; -
DR EMBL; AF523288; AAM74983.1; -
DR EMBL; AF523289; AAM74984.1; -
DR EMBL; AF523290; AAM74985.1; -
DR EMBL; AF523293; AAM74988.1; -
DR EMBL; AF523294; AAM74989.1; -
DR EMBL; AF523295; AAM74990.1; -
DR EMBL; AF523296; AAM74991.1; -
DR EMBL; AF523297; AAM74992.1; -
DR EMBL; AY253269; AAO86773.1; -
DR EMBL; AY253270; AAO86774.1; -
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR001064; Crystallin.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig MHC.
DR InterPro; IPR001039; MHC_I.
DR Pfam; PF00047; Ig; 1.
DR Pfam; PF00129; MHC_I; 1.
DR PRINTS; PR01638; MHCCLASSI.
DR PRODOM; PD000050; MHC_I; 1.
DR PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; 1.
DR PROSITE; PS00835; IG LIKE; 1.
DR PROSITE; PS00290; IG_MHC; 1.
SQ SEQUENCE 346 AA; 39051 MW; D4782AA4697D57B2 CRC64;

Query Match 100.0%; Score 1496; DB 7; Length 346;
Best Local Similarity 100.0%; Pred. No. 2.9e-122;

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Matches 274; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSHSLRYFSTAVSRGRGEPRIYAVYVDDTQFLRFDSDAAIPRMEPREPWWVEQGPQYW 60
DB 22 GSHSLRYFSTAVSRGRGEPRIYAVYVDDTQFLRFDSDAAIPRMEPREPWWVEQGPQYW 81
QY 61 EWTGTGAKANAQTDVALNLLRRYNQSEAGSHTLQGMNGCDMGPDGRLLRGYHQAHDG 120
DB 82 EWTGTGAKANAQTDVALNLLRRYNQSEAGSHTLQGMNGCDMGPDGRLLRGYHQAHDG 141
QY 121 KYISLNEDLSRWSAADTVAQITQRFYEAEBYAEFRTYLEGECLLELLRRLYENGKETLQ 180
DB 142 KYISLNEDLSRWSAADTVAQITQRFYEAEBYAEFRTYLEGECLLELLRRLYENGKETLQ 201
QY 181 RADPPKAHVAHPISDHEATLRCWALGFYPAEITLTWQDGEEOQDTLVELVETRPAGDGT 240
DB 202 RADPPKAHVAHPISDHEATLRCWALGFYPAEITLTWQDGEEOQDTLVELVETRPAGDGT 261
QY 241 FQKWAAVVPSGEEQRYTCHVQHEGLPQPLILRW 274
DB 262 FQKWAAVVPSGEEQRYTCHVQHEGLPQPLILRW 295

RESULT 4
Q95HCO PRELIMINARY; PRT; 442 AA.
ID Q95HCO AC Q95HCO
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Similar to major histocompatibility complex, class I, F.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung carcinoma;
RA Strausberg R.;
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC09260.1; -.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0008955; P: immune response; IEA.
DR InterPro; IPR001064; CRYSTALLIN.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR001039; MHC_I.
DR Pfam; PF00047; Ig; 1.
DR Pfam; PF00129; MHC_I; 1.
DR PRINTS; PR01638; MHCCLASSI.
DR ProDom; PD000050; MHC_I; 1.
DR SMART; SM00407; IGC1; 1.
DR PROSITE; PS00225; CRYSTALLIN BETAGAMMA; 1.
DR PROSITE; PS0835; IG LIKE; 1.
DR PROSITE; PS00290; IG_MHC; 1.
KW MHC.
SQ SEQUENCE 442 AA; 50427 MW; 6459D3B5F4B5704A CRC64;

Query Match 100.0%; Score 1496; DB 7; Length 442;
Best Local Similarity 100.0%; Pred. No. 4.1e-122;
Matches 274; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSHSLRYFSTAVSRGRGEPRIYAVYVDDTQFLRFDSDAAIPRMEPREPWWVEQGPQYW 60
DB 22 GSHSLRYFSTAVSRGRGEPRIYAVYVDDTQFLRFDSDAAIPRMEPREPWWVEQGPQYW 81
QY 61 EWTGTGAKANAQTDVALNLLRRYNQSEAGSHTLQGMNGCDMGPDGRLLRGYHQAHDG 120
DB 82 EWTGTGAKANAQTDVALNLLRRYNQSEAGSHTLQGMNGCDMGPDGRLLRGYHQAHDG 141
QY 121 KYISLNEDLSRWSAADTVAQITQRFYEAEBYAEFRTYLEGECLLELLRRLYENGKETLQ 180
DB 142 KYISLNEDLSRWSAADTVAQITQRFYEAEBYAEFRTYLEGECLLELLRRLYENGKETLQ 201
QY 181 RADPPKAHVAHPISDHEATLRCWALGFYPAEITLTWQDGEEOQDTLVELVETRPAGDGT 240
DB 202 RADPPKAHVAHPISDHEATLRCWALGFYPAEITLTWQDGEEOQDTLVELVETRPAGDGT 261
QY 241 FQKWAAVVPSGEEQRYTCHVQHEGLPQPLILRW 274
DB 262 FQKWAAVVPSGEEQRYTCHVQHEGLPQPLILRW 295

RESULT 5
Q8MGQ1 PRELIMINARY; PRT; 346 AA.
ID Q8MGQ1 AC Q8MGQ1
DT 01-OCT-2002 (TREMBLrel. 22, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE MHC class Ib antigen.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Ishitani A.; Miki A.; Williams L.M.; Moore Y.; Geraghty D.E.;
RT "HLA-E, F, and G polymorphism: genomic sequence defines new variation spanning the nonclassical class I genes."
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE IMMUNE SYSTEM (BY SIMILARITY).
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN) (BY SIMILARITY).
DR EMBL; AF523284; AAM74979.1; -.
DR EMBL; AF523291; AAM74986.1; -.
DR EMBL; AF523292; AAM74987.1; -.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0006955; P: immune response; IEA.
DR InterPro; IPR001064; CRYSTALLIN.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR001039; MHC_I.
DR Pfam; PF00047; Ig; 1.
DR Pfam; PF00129; MHC_I; 1.
DR PRINTS; PR01638; MHCCLASSI.
DR ProDom; PD000050; MHC_I; 1.
DR SMART; SM00407; IGC1; 1.
DR PROSITE; PS00225; CRYSTALLIN BETAGAMMA; 1.
DR PROSITE; PS0835; IG LIKE; 1.
DR PROSITE; PS00290; IG_MHC; 1.
KW Glycoprotein; Transmembrane.
SQ SEQUENCE 346 AA; 39061 MW; D4782968A67E9B7D CRC64;

Query Match 99.7%; Score 1491; DB 7; Length 346;
Best Local Similarity 99.6%; Pred. No. 7.9e-122;
Matches 273; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GSHSLRYFSTAVSRGRGEPRIYAVYVDDTQFLRFDSDAAIPRMEPREPWWVEQGPQYW 60
DB 22 GSHSLRYFSTAVSRGRGEPRIYAVYVDDTQFLRFDSDAAIPRMEPREPWWVEQGPQYW 81
QY 61 EWTGTGAKANAQTDVALNLLRRYNQSEAGSHTLQGMNGCDMGPDGRLLRGYHQAHDG 120
DB 82 EWTGTGAKANAQTDVALNLLRRYNQSEAGSHTLQGMNGCDMGPDGRLLRGYHQAHDG 141
QY 121 KYISLNEDLSRWSAADTVAQITQRFYEAEBYAEFRTYLEGECLLELLRRLYENGKETLQ 180
DB 142 KYISLNEDLSRWSAADTVAQITQRFYEAEBYAEFRTYLEGECLLELLRRLYENGKETLQ 201
QY 181 RADPPKAHVAHPISDHEATLRCWALGFYPAEITLTWQDGEEOQDTLVELVETRPAGDGT 240
DB 202 RADPPKAHVAHPISDHEATLRCWALGFYPAEITLTWQDGEEOQDTLVELVETRPAGDGT 261
QY 241 FQKWAAVVPSGEEQRYTCHVQHEGLPQPLILRW 274
DB 262 FQKWAAVVPSGEEQRYTCHVQHEGLPQPLILRW 295

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Db 202 RADPPKAAVHAHPISDHEATLRCWALGFYPABITLTWQDGEQOTDTLVELVETRPAGDGT 261
QY 241 FQKAAVAVVPSGEEQRYTCHVQHEGLPQPLILRW 274
Db 262 FQKAAVAVVPSGEEQRYTCHVQHEGLPQPLILRW 295

RESULT 6
Q9TP68 PRELIMINARY; PRT; 362 AA.
AC Q9TP68;
DT 01-MAY-2000 (T-EMBLrel. 13, Created)
DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE DJ377H14.9 (Major histocompatibility complex, class I, F
(CDA12)).
GN HLA-F.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Williams S.;
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE
IMMUNE SYSTEM (BY SIMILARITY).
CC -1- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
MICROGLOBULIN) (BY SIMILARITY).
DR EMBL; AL022723; CAB4623.1; -.
DR HSSP; Q30201; IA6Z.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR001064; Crystallin.
DR InterPro; IPR001104; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR001039; MHC_I.
DR Pfam; PF00047; Ig; 1.
DR Pfam; PF00129; MHC_I; 1.
DR PRINTS; PR01638; MHCCLASSI.
DR ProDom; PD000050; MHC_I; 1.
DR SMART; SM00407; IGc1; 1.
DR PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; 1.
DR PROSITE; PS00835; IG LIKE; 1.
DR PROSITE; PS00290; IG_MHC; 1.
KW Glycoprotein; Transmembrane.
SQ SEQUENCE 362 AA; 40578 MW; 970D072C813A07E2 CRC64;

Query Match 99.7%; Score 1491; DB 7; Length 362;
Best Local Similarity 99.6%; Pred. No. 8.4e-12; Mismatches 1; Indels 0; Gaps 0;
Matches 273; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GSHSLRYFSTAVSRPGEGEPRYIAVEYVDDTQFLRFDSDAAIPRMEPREPWVEQGPQYW 60
Db 22 GSHSLRYFSTAVSRPGEGEPRYIAVEYVDDTQFLRFDSDAAIPRMEPREPWVEQGPQYW 81

QY 61 EWTGAKANAQTDRAVLRNLLRRYNQSEAGSHTLQGMGCDMGPDGRLRGYHQHAYDG 120
Db 82 EWTGAKANAQTDRAVLRNLLRRYNQSEAGSHTLQGMGCDMGPDGRLRGYHQHAYDG 141

QY 121 KDYISLNEDLSRWTAADVAQITQRFYAEAYAEFRYLEGECLELLRRYLENGKETLQ 180
Db 142 KDYISLNEDLSRWTAADVAQITQRFYAEAYAEFRYLEGECLELLRRYLENGKETLQ 201

QY 181 RADPPKAAVHAHPISDHEATLRCWALGFYPABITLTWQDGEQOTDTLVELVETRPAGDGT 240
Db 202 RADPPKAAVHAHPISDHEATLRCWALGFYPABITLTWQDGEQOTDTLVELVETRPAGDGT 261

QY 241 FQKAAVAVVPSGEEQRYTCHVQHEGLPQPLILRW 274
Db 262 FQKAAVAVVPSGEEQRYTCHVQHEGLPQPLILRW 295

RESULT 8
Q7YR27 PRELIMINARY; PRT; 362 AA.
AC Q7YR27;
DT 01-OCT-2003 (T-EMBLrel. 25, Created)
DT 01-OCT-2003 (T-EMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Class ID.
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RESULT 7
Q95IT2 PRELIMINARY; PRT; 346 AA.
AC Q95IT2;
DT 01-DEC-2001 (T-EMBLrel. 19, Created)
DT 01-DEC-2001 (T-EMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE MHC class I antigen.
GN PATR-F.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21291697; PubMed=11398964;
RA Adams E.J.; Farham P.;
RT "Genomic analysis of common chimpanzee major histocompatibility
complex class I genes.";
RL Immunogenetics 53:200-208(2001).
DR EMBL; AF338355; AAK77479.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR001064; Crystallin.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR001039; MHC_I.
DR Pfam; PF00047; Ig; 1.
DR Pfam; PF00129; MHC_I; 1.
DR PRINTS; PR01638; MHCCLASSI.
DR ProDom; PD000050; MHC_I; 1.
DR SMART; SM00407; IGc1; 1.
DR PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; 1.
DR PROSITE; PS00835; IG LIKE; 1.
DR PROSITE; PS00290; IG_MHC; 1.
KW MHC.
SQ SEQUENCE 346 AA; 39009 MW; 0ECF12B7DB17B814 CRC64;

Query Match 98.7%; Score 1477; DB 7; Length 346;
Best Local Similarity 99.3%; Pred. No. 1.3e-12;
Matches 272; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GSHSLRYFSTAVSRPGEGEPRYIAVEYVDDTQFLRFDSDAAIPRMEPREPWVEQGPQYW 60
Db 22 GSHSLRYFSTAVSRPGEGEPRYIAVEYVDDTQFLRFDSDAAIPRMEPREPWVEQGPQYW 81

QY 61 EWTGAKANAQTDRAVLRNLLRRYNQSEAGSHTLQGMGCDMGPDGRLRGYHQHAYDG 120
Db 82 EWTGAKANAQTDRAVLRNLLRRYNQSEAGSHTLQGMGCDMGPDGRLRGYHQHAYDG 141

QY 121 KDYISLNEDLSRWTAADVAQITQRFYAEAYAEFRYLEGECLELLRRYLENGKETLQ 180
Db 142 KDYISLNEDLSRWTAADVAQITQRFYAEAYAEFRYLEGECLELLRRYLENGKETLQ 201

QY 181 RADPPKAAVHAHPISDHEATLRCWALGFYPABITLTWQDGEQOTDTLVELVETRPAGDGT 240
Db 202 RADPPKAAVHAHPISDHEATLRCWALGFYPABITLTWQDGEQOTDTLVELVETRPAGDGT 261

QY 241 FQKAAVAVVPSGEEQRYTCHVQHEGLPQPLILRW 274
Db 262 FQKAAVAVVPSGEEQRYTCHVQHEGLPQPLILRW 295

RESULT 8
Q7YR27 PRELIMINARY; PRT; 362 AA.
AC Q7YR27;
DT 01-OCT-2003 (T-EMBLrel. 25, Created)
DT 01-OCT-2003 (T-EMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Class ID.
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GN PATR-F.  
OS Pan troglodytes (Chimpanzee).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.  
OX NCBI\_TaxID=9598;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22709134; PubMed=12799463;  
RA Anzai T., Shiina T., Kimura N., Yanagiya K., Kohara S., Shigenari A.,  
RA Yamagata T., Kuletski J.K., Naruse T.K., Fujimori Y., Fukuzumi Y.,  
RA Yamazaki M., Tashiro H., Iwamoto C., Umehara Y., Imanishi T.,  
RA Meyer A., Ikeo K., Gojobori T., Bahram S., Inoko H.;  
RT "Comparative sequencing of human and chimpanzee MHC class I regions  
unveils insertions/deletions as the major path to genomic  
divergence."  
RI Proc. Natl. Acad. Sci. U.S.A. 100:7708-7713 (2003).  
RL EMBL; AB100087; BAC78191.1; -.  
DR EMBL; 362 AA; 40625 NW; BA5699D08181A1FF CRC64;  
SQ SEQUENCE 362 AA; 40625 NW; BA5699D08181A1FF CRC64;  
  
Query Match 98.7%; Score 1477; DB 6; Length 362;  
Best Local Similarity 99.3%; Pred. No. 1.4e-120; Indels 0; Gaps 0;  
Matches 272; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 1 GSHSLRYFSTAVSRGGRGEPRIAYEYVDDTQFLRFDSDAAI PRMEPREPWVEQGPQYW 60  
Db 22 GSHSLRYFSTAVSRGGRGEPRIAYEYVDDTQFLRFDSDAAI PRMEPREPWVEQGPQYW 81  
  
QY 61 EHTTGYAKANAQTDVALNLLRRYNOSEAGSHTLQMGNGCDMGDPGRLRGYHCHAYDG 120  
Db 82 EHTTGYAKANAQTDVALNLLRRYNOSEAGSHTLQMGNGCDMGDPGRLRGYHCHAYDG 141  
  
QY 121 KDYISLNEDLRSWTAADTVAQITQRFYEAEEYAEAEFRYLEGECELELLRRYLENGKETLQ 180  
Db 142 KDYISLNEDLRSWTAADTVAQITQRFYEAEEYAEAEFRYLEGECELELLRRYLENGKETLQ 201  
  
QY 181 RADPPKARVAHPISDHEATLRCWALGFYPABITLTWQDGEQOTDELVELVETRPAGDGT 240  
Db 202 RADPPKARVAHPISDHEATLRCWALGFYPABITLTWQDGEQOTDELVELVETRPAGDGT 261  
  
QY 241 FOKWAAVVPSGGEORVYCHVQHEGLPQLTLRW 274  
Db 262 FOKWAAVVPSGGEORVYCHVQHEGLPQLTLRW 295  
  
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O19692 PRELIMINARY; PRT; 274 AA.  
ID O19692  
AC O19692  
DT 01-JAN-1998 (TrEMBLrel. 05, Created)  
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE HLA-B protein (Fragment).  
GN HLA-B.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=87009855; PubMed=3489755;  
RA Coppin H.L., McDavitt H.O.;  
RT "Absence of polymorphism between HLA-B\*27 genomic exon sequences  
isolated from normal donors and ankylosing spondylitis patients."  
RL J. Immunol. 137:2168-2172 (1986).  
CC -1- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE  
IMMUNE SYSTEM (BY SIMILARITY).  
CC -1- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-  
MICROGLOBULIN) (BY SIMILARITY).  
CC EMBL; M14013; AAA59643.1; -.  
DR HSSP; P03989; 1HSA.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0006955; P:immune response; IEA.  
DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003597; Ig cl.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR001039; MHC\_I.  
DR Pfam; PF00047; Ig; 1.  
DR Pfam; PF00129; MHC\_I; 1.  
DR PRINTS; PR01638; MHCCLASSI.  
DR ProDom; PD000050; MHC\_I; 1.  
DR SMART; SM00407; IGcl; 1.  
DR PROSITE; PS00835; IG\_LIKE; 1.  
DR PROSITE; PS00290; IG\_MHC; 1.  
KW Glycoprotein; Transmembrane.  
FT NON TER 1  
FT NON TER 274 274  
SQ SEQUENCE 274 AA; 31659 MW; OC9A7A4902383219 CRC64;  
  
Query Match 82.9%; Score 1240; DB 7; Length 274;  
Best Local Similarity 82.8%; Pred. No. 4.6e-100;  
Matches 227; Conservative 14; Mismatches 33; Indels 0; Gaps 0;  
  
QY 1 GSHSLRYFSTAVSRGGRGEPRIAYEYVDDTQFLRFDSDAAI PRMEPREPWVEQGPQYW 60  
Db 1 GSHSLRYFSTAVSRGGRGEPRIAYEYVDDTQFLRFDSDAAI PRMEPREPWVEQGPQYW 60  
  
QY 61 EHTTGYAKANAQTDVALNLLRRYNOSEAGSHTLQMGNGCDMGDPGRLRGYHCHAYDG 120  
Db 61 DRETQICAKAQTDREDLRLRLRYNOSEAGSHTLQMGNGCDMGDPGRLRGYHCHAYDG 120  
  
QY 121 KDYISLNEDLRSWTAADTVAQITQRFYEAEEYAEAEFRYLEGECELELLRRYLENGKETLQ 180  
Db 121 KDYISLNEDLRSWTAADTVAQITQRFYEAEEYAEAEFRYLEGECELELLRRYLENGKETLQ 180  
  
QY 181 RADPPKARVAHPISDHEATLRCWALGFYPABITLTWQDGEQOTDELVELVETRPAGDGT 240  
Db 181 RADPPKARVAHPISDHEATLRCWALGFYPABITLTWQDGEQOTDELVELVETRPAGDGT 240  
  
QY 241 FOKWAAVVPSGGEORVYCHVQHEGLPQLTLRW 274  
Db 241 FOKWAAVVPSGGEORVYCHVQHEGLPQLTLRW 274  
  
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RESULT 10  
P79612 PRELIMINARY; PRT; 362 AA.  
ID P79612  
AC P79612  
DT 01-MAY-1997 (TrEMBLrel. 03, Created)  
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE HLA-B protein.  
GN HLA-B.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Blood.  
RA Hasegawa T., Sugahara Y., Moriyama Y., Nanzai H., Ogawa A., Tawara K.,  
RA Kondo S., Tokunaga K.;  
RT "Molecular characterization of a novel HLA-B\*27 allele."  
RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.  
CC -1- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE  
IMMUNE SYSTEM (BY SIMILARITY).  
CC -1- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-  
MICROGLOBULIN) (BY SIMILARITY).  
CC EMBL; D83043; BAA11753.1; -.  
DR HSSP; P03989; 1HSA.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0006955; P:immune response; IEA.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig cl.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR001039; MHC\_I.  
DR Pfam; PF00047; Ig; 1.

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DR Pfam; PF00129; MHC_I; 1.
DR PRINTS; PR01638; MHCCLASSI.
DR ProDom; PD000050; MHC_I; 1.
DR SMART; SMC0407; IGC1; 1.
DR PROSITE; PS00835; IG LIKE; 1.
DR PROSITE; PS00290; IG_MHC; 1.
KW Glycoprotein; Transmembrane.
SQ SEQUENCE 362 AA; 4041 MW; 3CA5547E65FDF84 CRC64;

Query Match 82.9%; Score 1240; DB 7; Length 362;
Best Local Similarity 82.5%; Pred. No. 6.8e-100;
Matches 226; Conservative 19; Mismatches 30; Indels 0; Gaps 0;

QY 1 GSHSLRYFSTAVSRPGRGEPRIYAVYDDTQFLRFDSDAAIPRMEPREPWEQEGPOYW 60
DB 25 GSHSMRYFHTSVSRPGRGEPRIYVGYDDTLFVRFDSDAASPREPRAPWIEQEGPEYW 84
QY 61 EWTTCYAKANAQTDRLVALNLLRRYNQSEAGSHTLQGMNGCDMPDGRLLRGYHQAYDG 120
DB 85 DRETQICKAKAQTDRLSLRTLRLRYNQSEAGSHTLQSMYGCVDGPDGRLLRGHNOYAYDG 144
QY 121 KOVISLNEDLRSWTAADTAQITQRFYEAEEYAEFRTYLEGCELELLRRYLENGKETLQ 180
DB 145 KOYIALNEDLRSWTAADTAQITQRKWEARVAEQRLAYLEGCEVSWLRYLENGKETLQ 204
QY 181 RADPPKAHVAHPISDHEATLRCWALGFYPAEITLTWQDGEBOQTQDTLVEPRAGDGT 240
DB 205 RADPPKTHVTHHPISDHEATLRCWALGFYPAEITLTWQDGEDQTDQDTLVEPRAGDRT 264
QY 241 FQKWAAVVPSGEGORYTCHVQHEGLPOPLILRW 274
DB 265 FQKWAAVVPSGEGORYTCHVQHEGLPKPLTLRW 298

RESULT 11
Q78189 PRELIMINARY; PRT; 362 AA.
AC Q78189;
DT 01-NOV-1998 (T-EMBLrel. 08, Created)
DT 01-NOV-1998 (T-EMBLrel. 08, Last sequence update)
DE 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE MHC class I antigen.
GN HLA-B.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98427840; PubMed=9756409;
RA Seurynck K., Baxter-Lowe L.A.;
RT "Novel polymorphism detected in exon 1 of HLA-B*2713."
RL Tissue Antigens 52:187-189(1998).
CC -1- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE
CC IMMUNE SYSTEM (BY SIMILARITY).
CC -1- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN) (BY SIMILARITY).
CC EMBL; AF026218; AAC42275.1; -.
DR HSSP; P03989; 1HSA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; IG_MHC.
DR Pfam; PF00047; Ig; 1.
DR PRINTS; PR01638; MHCCLASSI.
DR ProDom; PD000050; MHC_I; 1.
DR SMART; SMC0407; IGC1; 1.
DR PROSITE; PS00290; IG_MHC; 1.
KW Glycoprotein; Transmembrane.
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SQ SEQUENCE 362 AA; 40486 MW; BCO0FC372955711D CRC64;

Query Match 82.9%; Score 1240; DB 7; Length 362;
Best Local Similarity 82.8%; Pred. No. 6.8e-100;
Matches 227; Conservative 14; Mismatches 33; Indels 0; Gaps 0;

QY 1 GSHSLRYFSTAVSRPGRGEPRIYAVYDDTQFLRFDSDAAIPRMEPREPWEQEGPOYW 60
DB 25 GSHSMRYFHTSVSRPGRGEPRIYVGYDDTLFVRFDSDAASPREPRAPWIEQEGPEYW 84
QY 61 EWTTCYAKANAQTDRLVALNLLRRYNQSEAGSHTLQGMNGCDMPDGRLLRGYHQAYDG 120
DB 85 DRETQICKAKAQTDRLSLRTLRLRYNQSEAGSHTLQNMVYGCVDGPDGRLLRGYHQAYDG 144
QY 121 KOVISLNEDLRSWTAADTAQITQRFYEAEEYAEFRTYLEGCELELLRRYLENGKETLQ 180
DB 145 KOYIALNEDLRSWTAADTAQITQRKWEARVAEQRLAYLEGCEVSWLRYLENGKETLQ 204
QY 181 RADPPKAHVAHPISDHEATLRCWALGFYPAEITLTWQDGEBOQTQDTLVEPRAGDGT 240
DB 205 RADPPKTHVTHHPISDHEATLRCWALGFYPAEITLTWQDGEDQTDQDTLVEPRAGDRT 264
QY 241 FQKWAAVVPSGEGORYTCHVQHEGLPOPLILRW 274
DB 265 FQKWAAVVPSGEGORYTCHVQHEGLPKPLTLRW 298

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Q29705 PRELIMINARY; PRT; 362 AA.
AC Q29705;
DT 01-NOV-1996 (T-EMBLrel. 01, Created)
DT 01-NOV-1996 (T-EMBLrel. 01, Last sequence update)
DE 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)
DE MHC class I antigen HLA-B precursor.
GN HLA-B.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Blood;
RA Balas A., Santos S., Vicario J.L.;
RT "Serological and molecular characterization of a novel HLA-B allele."
RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; U31971; AAA98506.1; -.
DR HSSP; P03989; 1HSA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR001039; MHC_I.
DR Pfam; PF00047; Ig; 1.
DR Pfam; PF00129; MHC_I; 1.
DR PRINTS; PR01638; MHCCLASSI.
DR ProDom; PD000050; MHC_I; 1.
DR SMART; SMC0407; IGC1; 1.
DR PROSITE; PS00290; IG_MHC; 1.
KW SIGNAL.
FT SIGNAL.
FT CHAIN.
SQ SEQUENCE 362 AA; 40479 MW; 148B5656159EA505 CRC64;

Query Match 82.8%; Score 1239; DB 4; Length 362;
Best Local Similarity 82.5%; Pred. No. 8.3e-100;
Matches 226; Conservative 16; Mismatches 32; Indels 0; Gaps 0;

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DB 25 GSHSMRYFHTSVSRPGRGEPRIYVGYDDTLFVRFDSDAASPREPRAPWIEQEGPEYW 84
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DB	25	GSQSMRYEYTTAMSPRGCEPPIAVGYDDTQFVRFDSDAALPRMEPRAPWLEQSGPEYW	84		
QY	61	EWTCYAKANAQTORVALRNILLRRYNQSEAGSHTLQGNMGCDMGPDGRLLRGYHQAQYD	120		
DB	85	DRNTQGIKTQACTDRENTLTLRYYNQSEAGSHTLQSMYGCMDGPDGRLLRGYDQYAYD	144		

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DB 145 KDYIALNKDLSSTAAADTAAQITQRFYEAEEVAEPEPTYLEGECLELLRRYLENGKETLQ 204  
QY 181 RADPPKAAHVAHPISDHEATLRCWALGFYPAEITLTWQDGEOTQDTLTVETRPAGDGT 240  
DB 205 RADPPKTHVTHHPISDHEATLRCWALGFYPAEITLTWQDGEOTQDTLTVETRPAGDRT 264  
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DB 265 FOKWAAVVVPSGEGEORYTCHVQHEGLPQPLILRW 298

RESULT 15

Q29934  
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AC Q29934;  
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DT 01-NOV-1996 (T-EMBLrel. 01, Last sequence update)  
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)  
DE HLA-B protein (Fragment).  
GN HLA-B.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP MEDLINE=86149317; PubMed=3485286;  
RA Szöcs H., Riethmüller G., Weiss E., Meo T.;  
RT "Complete sequence of HLA-B\*27 cDNA identified through the  
RT characterization of structural markers unique to the HLA-A, -B, and -C  
RT allelic series.";  
RL Proc. Natl. Acad. Sci. U.S.A. 83:1428-1432(1986).  
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE  
CC IMMUNE SYSTEM (BY SIMILARITY).  
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-  
CC MICROGLOBULIN) (BY SIMILARITY).  
DR EMBL; M12678; AA59614.1; -;  
DR HSP; P03989; IHS.  
DR GO; GO:0016021; C: integral to membrane; IEA.  
DR GO; GO:0006955; P: immune response; IEA.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig cl.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR001039; MHC\_I.  
DR Pfam; PF00047; Ig; 1.  
DR Pfam; PF00129; MHC\_I; 1.  
DR PRINTS; PR01638; MHCCLASSI.  
DR PRODOM; PD000050; MHC\_I; 1.  
DR SMART; SM00407; IGcl; 1.  
DR PROSITE; PS00835; IG\_LIKE; 1.  
DR PROSITE; PS00290; IG\_MHC; 1.  
KW Glycoprotein; Transmembrane.  
FT NON TER 1  
SQ SEQUENCE 359 AA; 40042 MW; 65B534A8980E7A88 CRC64;

Query Match 82.6%; Score 1236; DB 7; Length 359;  
Best Local Similarity 82.5%; Pred. No. 1.5e-99;  
Matches 226; Conservative 14; Mismatches 34; Indels 0; Gaps 0;

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DB 22 GSHSMRYFHTSVSRPGEGEPYITGVYVDDTFLVRFDSDAASPREEPAPWIEQEGPEY 81  
QY 61 EWTGYAKANAQTORVALNRLRRYNQSEAGSHLTQGMNGCDMGPDGRLLRGVHODYDG 120  
DB 82 DRETQICAKAQTDREDLRLRYNQSEAGSHLTQGMNGCDVGPDLRLRGVHODYDG 141  
QY 121 KDYISLNEDLSRSTAADTVAQITQRFYEAEEVAEPEPTYLEGECLELLRRYLENGKETLQ 180  
DB 142 KDYIALNKDLSSTAAADTAAQITQRFYEAEEVAEPEPTYLEGECLELLRRYLENGKETLQ 201

QY 181 RADPPKAAHVAHPISDHEATLRCWALGFYPAEITLTWQDGEOTQDTLTVETRPAGDGT 240  
DB 202 RVDPEKTHVTHHPISDHEATLRCWALGFYPAEITLTWQDGEOTQDTLTVETRPAGDRT 261  
QY 241 FOKWAAVVVPSGEGEORYTCHVQHEGLPQPLILRW 274  
DB 262 FOKWAAVVVPSGEGEORYTCHVQHEGLPQPLILRW 295

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Job time : 47 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 18, 2004, 19:31:27 ; Search time 48 Seconds  
(without alignments)  
1611.540 Million cell updates/sec

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Perfect score: 274

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Gapop 60.0 , Gapext 60.0

Searched: 1163542 segs, 282313646 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1163542

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published Applications AA.\*

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- 18: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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2	274	100.0	362	12	US-10-257-021-82
3	274	100.0	442	16	US-10-408-765A-1887
4	241	88.0	271	9	US-09-925-301-1431
5	175	63.9	362	12	US-09-819-371-4
6	119	43.4	215	12	US-09-819-371-6
7	70	25.5	186	15	US-10-264-049-4063
8	68	24.8	96	14	US-10-029-386-30718
9	44	16.1	77	14	US-10-029-386-34273
10	44	16.1	91	14	US-10-029-386-31089
11	44	16.1	104	9	US-09-925-302-835
12	44	16.1	104	12	US-09-925-302-835
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14	40	14.6	371	12	US-10-210-172-156
15	40	14.6	371	15	US-10-085-198-72

16	39	14.2	91	9	US-09-864-761-38005	Sequence 38005, A
17	39	14.2	92	12	US-10-380-880-5	Sequence 5, Appli
18	39	14.2	234	12	US-10-380-880-8	Sequence 8, Appli
19	39	14.2	284	15	US-10-104-047-3648	Sequence 3648, Ap
20	39	14.2	326	12	US-10-380-880-7	Sequence 7, Appli
21	39	14.2	379	12	US-10-210-172-160	Sequence 160, App
22	39	14.2	379	15	US-10-093-463-78	Sequence 78, Appli
23	38	13.9	145	9	US-09-810-560-8	Sequence 8, Appli
24	36	13.1	45	14	US-10-029-386-28883	Sequence 28883, A
25	32	11.7	91	9	US-09-864-761-35461	Sequence 35461, A
26	32	11.7	110	9	US-09-796-692-799	Sequence 799, App
27	32	11.7	110	9	US-09-796-692-2139	Sequence 2139, App
28	32	11.7	110	14	US-10-040-862-799	Sequence 799, App
29	32	11.7	110	14	US-10-040-862-2139	Sequence 2139, App
30	32	11.7	110	15	US-10-057-475B-799	Sequence 799, App
31	32	11.7	110	15	US-10-057-475B-2139	Sequence 2139, App
32	32	11.7	110	15	US-10-154-884B-799	Sequence 799, App
33	32	11.7	110	15	US-10-154-884B-2139	Sequence 2139, App
34	32	11.7	196	12	US-10-262-839-48	Sequence 48, Appli
35	32	11.7	198	15	US-10-264-049-3505	Sequence 3505, Ap
36	29	10.6	280	14	US-10-073-300-6	Sequence 6, Appli
37	29	10.6	280	15	US-10-075-257-6	Sequence 6, Appli
38	29	10.6	365	14	US-10-138-888-23	Sequence 23, Appli
39	29	10.6	389	12	US-10-108-511-2	Sequence 2, Appli
40	29	10.6	415	14	US-10-073-300-5	Sequence 5, Appli
41	29	10.6	415	16	US-10-075-257-5	Sequence 5, Appli
42	29	10.6	510	12	US-10-108-511-5	Sequence 5, Appli
43	28	10.2	96	14	US-10-029-386-28377	Sequence 28377, A
44	23	8.4	117	9	US-09-810-560-9	Sequence 9, Appli
45	23	8.4	361	14	US-10-138-888-22	Sequence 22, Appli

#### ALIGNMENTS

#### RESULT 1

US-09-819-371-5  
; Sequence 5, Application US/09819371  
; Publication No. US20040053344A1  
; GENERAL INFORMATION:  
; APPLICANT: Egawa, Kohji  
; TITLE OF INVENTION: Cancer Cell-Specific HLA-F Antigen and a Diagnostic Method of Ca  
; FILE REFERENCE: 30815  
; CURRENT APPLICATION NUMBER: US/09/819,371  
; CURRENT FILING DATE: 2002-03-15  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 5  
; LENGTH: 274  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-819-371-5

Query Match 100.0%; Score 274; DB 12; Length 274;  
Best Local Similarity 100.0%; Pred. No. 3.8e-265;  
Matches 274; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	GSHSLRYFSTAVSRPGRGPRIAYEYVDDTQFLRFDSDAAI PRMEPREPWEQGPQYW	60
Db	1	GSHSLRYFSTAVSRPGRGPRIAYEYVDDTQFLRFDSDAAI PRMEPREPWEQGPQYW	60
Qy	61	EWTTGYAKNAQTQVALNLLRRYNQSEAGSHTLQGNMGCDMGPDGRLLRGYHOAYDG	120
Db	61	EWTTGYAKNAQTQVALNLLRRYNQSEAGSHTLQGNMGCDMGPDGRLLRGYHOAYDG	120
Qy	121	KDYISLNDLSRWSAADTVAQITQRFYEAEYAEFFTYLEGECLLELLRRYLENGKETLQ	180
Db	121	KDYISLNDLSRWSAADTVAQITQRFYEAEYAEFFTYLEGECLLELLRRYLENGKETLQ	180
Qy	181	RADPPKAHVHHPISDHATLRCLWALGYPAEITLTITWQDGEETQDTVELVETRPAGDGT	240
Db	181	RADPPKAHVHHPISDHATLRCLWALGYPAEITLTITWQDGEETQDTVELVETRPAGDGT	240



```

RESULT 9
US-10-029-386-34273
; Sequence 34273, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Penn, Sharon G.
; APPLICANT: Penn, Sharon G.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
; FILE REFERENCE: AEOMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 34273
; LENGTH: 77
; TYPE: PRT

```

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 48  
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 11  
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 57  
OTHER INFORMATION: SWISSPROT HIT: P30507, EVALUE 7.00e-24  
US-10-029-386-30752

Query Match 14.6%; Score 40; DB 14; Length 78;  
Best Local Similarity 100.0%; Pred. No. 7.3e-32;  
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 228 TELVETRPAGDGTGFKWAAVVVPSGGEQRYTCHVQHEGLP 267  
DB 29 TELVETRPAGDGTGFKWAAVVVPSGGEQRYTCHVQHEGLP 68

RESULT 14  
US-10-210-172-156  
Sequence 156, Application US/10210172  
Publication No. US20040043928A1  
GENERAL INFORMATION:  
APPLICANT: Kekuda, Ramesh  
APPLICANT: Miller, Charles  
APPLICANT: Patturajan, Meera  
APPLICANT: Pena, Carol  
APPLICANT: Rieser, Daniel  
APPLICANT: Shmukets, Richard  
APPLICANT: Zernhusen, Bryan  
APPLICANT: Li, Li  
APPLICANT: Ji, Weizhen  
APPLICANT: Padigaru, Muralidhara  
APPLICANT: Casman, Stacie  
APPLICANT: Voss, Edward  
APPLICANT: Boldog, Ferenc  
APPLICANT: Gorman, Linda  
APPLICANT: Leite, Mario  
APPLICANT: Vernet, Corine  
APPLICANT: Anderson, David  
APPLICANT: Guo, Xiaojia  
APPLICANT: Zhong, Mei  
APPLICANT: Gerlach, Valerie  
APPLICANT: Hjal, Tor-d  
APPLICANT: Rastelli, Luca  
APPLICANT: Spytek, Kimberly  
APPLICANT: Edinger, Shlomit  
APPLICANT: Ellerman, Karen  
APPLICANT: Malyankar, Uriel  
APPLICANT: MacDougall, John  
APPLICANT: Stone, David  
APPLICANT: Alsobrook II, John  
APPLICANT: Lepley, Denise et al.  
TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHO  
FILE REFERENCE: 21402-416 A  
CURRENT APPLICATION NUMBER: US/10/210,172  
CURRENT FILING DATE: 2001-08-01  
PRIOR APPLICATION NUMBER: 60/309,501  
PRIOR FILING DATE: 2001-08-02  
PRIOR APPLICATION NUMBER: 60/323,994  
PRIOR FILING DATE: 2001-09-21  
PRIOR APPLICATION NUMBER: 60/373,814  
PRIOR FILING DATE: 2002-04-19  
PRIOR APPLICATION NUMBER: 60/310,291  
PRIOR FILING DATE: 2001-08-03  
PRIOR APPLICATION NUMBER: 60/310,951  
PRIOR FILING DATE: 2001-08-08  
PRIOR APPLICATION NUMBER: 60/310,544  
PRIOR FILING DATE: 2001-08-07  
PRIOR APPLICATION NUMBER: 60/311,292  
PRIOR FILING DATE: 2001-08-09  
PRIOR APPLICATION NUMBER: 60/311,979  
PRIOR FILING DATE: 2001-08-13  
PRIOR APPLICATION NUMBER: 60/313,201  
PRIOR FILING DATE: 2001-08-17  
PRIOR APPLICATION NUMBER: 60/312,892

ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: SITE  
LOCATION: (95)  
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
US-09-925-302-835

Query Match 16.1%; Score 44; DB 9; Length 104;  
Best Local Similarity 100.0%; Pred. No. 9.6e-36;  
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 224 QTQDTLTVETRPAGDGTGFKWAAVVVPSGGEQRYTCHVQHEGLP 267  
DB 32 QTQDTLTVETRPAGDGTGFKWAAVVVPSGGEQRYTCHVQHEGLP 75

RESULT 12  
US-09-925-302-835  
Sequence 835, Application US/09925302  
Publication No. US20030064072A9  
GENERAL INFORMATION:  
APPLICANT: Rozen et al.  
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies  
FILE REFERENCE: PA104  
CURRENT APPLICATION NUMBER: US/09/925,302  
CURRENT FILING DATE: 2001-08-10  
PRIOR APPLICATION NUMBER: PCT/US00/05918  
PRIOR FILING DATE: 2000-03-08  
PRIOR APPLICATION NUMBER: 60/124,270  
PRIOR FILING DATE: 1999-03-12  
NUMBER OF SEQ ID NOS: 896  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 835  
LENGTH: 104  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: SITE  
LOCATION: (95)  
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
US-09-925-302-835

Query Match 16.1%; Score 44; DB 12; Length 104;  
Best Local Similarity 100.0%; Pred. No. 9.6e-36;  
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 224 QTQDTLTVETRPAGDGTGFKWAAVVVPSGGEQRYTCHVQHEGLP 267  
DB 32 QTQDTLTVETRPAGDGTGFKWAAVVVPSGGEQRYTCHVQHEGLP 75

RESULT 13  
US-10-029-386-30752  
Sequence 30752, Application US/10029386  
Publication No. US20030194704A1  
GENERAL INFORMATION:  
APPLICANT: Penn, Sharron G.  
APPLICANT: Rank, David R.  
APPLICANT: Hanzel, David K.  
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G  
TITLE OF INVENTION: EXPRESSION ANALYSIS TWO  
FILE REFERENCE: AEMICA-X-2  
CURRENT APPLICATION NUMBER: US/10/029,386  
CURRENT FILING DATE: 2001-12-20  
NUMBER OF SEQ ID NOS: 34288  
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1  
SEQ ID NO 30752  
LENGTH: 78  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: MAP TO CHR6.1  
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 8.7

; PRIOR FILING DATE: 2001-08-16  
; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 327  
; SOFTWARE: Curasequest version 0.1

; SEQ ID NO 156

; LENGTH: 371

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-210-172-156

Query Match 14.6%; Score 40; DB 12; Length 371;  
Best Local Similarity 100.0%; Pred. No. 3e-31;  
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 228 TELVETRPAGDTGTFQKAAVVPSPGGEORYTCHVQHEGLP 267

Db 250 TELVETRPAGDTGTFQKAAVVPSPGGEORYTCHVQHEGLP 289

#### RESULT 15

US-10-085-198-72

; Sequence 72, Application US/10085198

; Publication No. US20040009907A1

; GENERAL INFORMATION:

; APPLICANT: Alsbrook et al.

; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same

; FILE REFERENCE: 21402-279

; CURRENT APPLICATION NUMBER: US/10/085,198

; CURRENT FILING DATE: 2002-02-25

; PRIOR APPLICATION NUMBER: 60/271,646

; PRIOR FILING DATE: 2001-02-26

; PRIOR APPLICATION NUMBER: 60/276,401

; PRIOR FILING DATE: 2001-03-16

; PRIOR APPLICATION NUMBER: 60/311,981

; PRIOR FILING DATE: 2001-08-13

; PRIOR APPLICATION NUMBER: 60/312,858

; PRIOR FILING DATE: 2001-08-16

; PRIOR APPLICATION NUMBER: 60/271,840

; PRIOR FILING DATE: 2001-02-27

; PRIOR APPLICATION NUMBER: 60/277,324

; PRIOR FILING DATE: 2001-03-20

; PRIOR APPLICATION NUMBER: 60/286,096

; PRIOR FILING DATE: 2001-04-21

; PRIOR APPLICATION NUMBER: 60/299,695

; PRIOR FILING DATE: 2001-06-20

; PRIOR APPLICATION NUMBER: 60/315,614

; PRIOR FILING DATE: 2001-08-29

; PRIOR APPLICATION NUMBER: 60/272,405

; PRIOR FILING DATE: 2001-02-28

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 653

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 72

; LENGTH: 371

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-085-198-72

Query Match 14.6%; Score 40; DB 15; Length 371;  
Best Local Similarity 100.0%; Pred. No. 3e-31;  
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 228 TELVETRPAGDTGTFQKAAVVPSPGGEORYTCHVQHEGLP 267

Db 250 TELVETRPAGDTGTFQKAAVVPSPGGEORYTCHVQHEGLP 289

Search completed: June 18, 2004, 19:37:21  
Job time : 49 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 18, 2004, 19:26:06 ; Search time 61 Seconds  
(without alignments)  
1269.148 Million cell updates/sec

Title: US-09-819-371-5  
Perfect score: 274  
Sequence: 1 GSHSLRVFSTAVSRGGRGP.....QRYTCHVQHEGLPOLILRW 274

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 1586107 seqs, 282547505 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : A\_Geneseq\_29Jan04:\*

- 1: geneseqp1980s:\*
- 2: geneseqp1990s:\*
- 3: geneseqp2000s:\*
- 4: geneseqp2001s:\*
- 5: geneseqp2002s:\*
- 6: geneseqp2003as:\*
- 7: geneseqp2003bs:\*
- 8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	274	100.0	274	4	AAG64618 Human can
2	274	100.0	362	4	AAG64617 Human can
3	274	100.0	362	4	AB50296 HLA-Cw ov
4	250	91.2	677	4	AB526726 Novel hum
5	241	88.0	271	3	AAB43986 Human can
6	215	78.5	215	4	AAG64619 Human can
7	99	36.1	120	3	AAG00209 Human sec
8	70	25.5	186	5	AB242931 Human ova
9	44	16.1	104	3	AB58497 Lung canc
10	44	16.1	104	3	AB58497 Lung canc
11	44	16.1	366	2	AAR12466 HLA-C exo
12	44	16.1	366	2	AAY07033 Breast ca
13	44	16.1	374	4	AAC13073 Human pol
14	44	16.1	380	4	AAC13073 Human pol
15	43	15.7	120	4	AAB90793 Novel hum
16	43	15.7	362	7	AB311177 Human she
17	40	14.6	371	7	AB311177 Human she
18	39	14.2	91	4	AB311177 Human she
19	39	14.2	91	4	AB311177 Human she
20	39	14.2	91	4	AB311177 Human she
21	39	14.2	91	4	AB311177 Human she
22	39	14.2	91	4	AB311177 Human she
23	39	14.2	91	4	AB311177 Human she
24	39	14.2	91	4	AB311177 Human she
25	39	14.2	91	4	AB311177 Human she

26	39	14.2	91	4	AAM05976 Peptide #
27	39	14.2	91	5	ABG40192 Human pep
28	39	14.2	92	5	Aau79452 HLA-G alp
29	39	14.2	234	5	Aau79455 HLA-G rec
30	39	14.2	284	7	ADB65494 Human pro
31	39	14.2	326	5	Aau79454 HLA-G rec
32	39	14.2	338	7	ADD46572 Human pro
33	39	14.2	379	5	ABP70087 Human NOV
34	39	14.2	379	7	ADE40254 Human NOV
35	32	11.7	91	4	AAM15751 Peptide #
36	32	11.7	91	4	ABB34748 Peptide #
37	32	11.7	91	4	AAM28260 Peptide #
38	32	11.7	91	4	ABB29570 Peptide #
39	32	11.7	91	4	ABB20163 Protein #
40	32	11.7	91	4	AAM67933 Human bon
41	32	11.7	91	4	AAM55549 Human bra
42	32	11.7	91	4	ABG49576 Human liv
43	32	11.7	91	4	AAM03485 Peptide #
44	32	11.7	91	5	ABG37468 Human pep
45	32	11.7	110	4	AAM81775 Human hae

ALIGNMENTS

RESULT 1  
AAG64618  
ID AAG64618 standard; protein; 274 AA.  
XX AAG64618;  
AC AAG64618;  
XX  
DT 12-SEP-2001 (first entry)  
XX  
DE Human cancer cell specific HLA-F antigen SEQ ID 5.  
XX  
KW HLA-F antigen; cancer cell specific; human.  
XX  
OS Homo sapiens.  
XX  
FN JP2001095584-A.  
XX  
PD 10-APR-2001.  
XX  
PF 30-SEP-1999; 99JP-00279566.  
XX  
PR 30-SEP-1999; 99JP-00279566.  
XX  
PA (EGAW/) EGAWA K.  
PA (MEDI-) MEDINET KK.  
PA (KIMU/) KIMURA K.  
XX  
DR WPI; 2001-360493/38.  
DR N-PSDB; AAH45556.  
XX  
FT Novel cancer cell-specific HLA-F antigen useful for diagnosing cancer.  
XX  
PS Claim 2; Page 10-11; 12pp; Japanese.  
XX  
CC This invention relates to a cancer cell specific HLA-F antigen. The  
CC invention includes DNA encoding the antigen, and a method for the  
CC preparation of the cancer cell specific HLA-F antigen. The antigen may be  
CC used in a method to diagnose cancer, in which the protein is used to  
CC detect anti-HLA-F antibodies in bodily fluids of the patient. The present  
CC sequence represents the cancer cell-specific HLA-F antigen of the  
CC invention  
XX  
SQ Sequence 274 AA;

Query Match 100.0%; Score 274; DB 4; Length 274;  
Best Local Similarity 100.0%; Pred. No. 5.3e-250;  
Matches 274; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GSHSLRVFSTAVSRGGRGP...RYTCHVQHEGLPOLILRW 60

Db 1 GSHSLRYSTAVSRGPRGEPYIAVEYVDDTQFLRFDSDAAIPRMEPRPWEQGPQYW 60  
 QY 61 EWTGAKANAQTRVALRNLRRYNQSEAGSHTLQGMNGCDMPDGRLLRGYHQHAYDG 120  
 Db 61 EWTGAKANAQTRVALRNLRRYNQSEAGSHTLQGMNGCDMPDGRLLRGYHQHAYDG 120  
 QY 121 KDYISLNEDLSRWTAAADTVAQITQRFYEAEBEYAEFFTYLEGECLLELLRRYLENGKETLQ 180  
 Db 121 KDYISLNEDLSRWTAAADTVAQITQRFYEAEBEYAEFFTYLEGECLLELLRRYLENGKETLQ 180  
 QY 181 RADPPKHAHVHPISDHEATLRCWALGFYPAEITLTWQRDGEQCTODTELVEVTRPAGDGT 240  
 Db 181 RADPPKHAHVHPISDHEATLRCWALGFYPAEITLTWQRDGEQCTODTELVEVTRPAGDGT 240  
 QY 241 FQKWAADVVPSEGEQRYTCHVQHEGLPOPLILRW 274  
 Db 241 FQKWAADVVPSEGEQRYTCHVQHEGLPOPLILRW 274  
 RESULT 2  
 AAG64617  
 ID AAG64617 standard; protein; 362 AA.  
 XX AC AAG64617;  
 XX DT 12-SEP-2001 (first entry)  
 XX DE Human cancer cell specific HLA-F antigen SEQ ID 4.  
 XX KW HLA-F antigen; cancer cell specific; human.  
 XX OS Homo sapiens.  
 XX FN JP2001095584-A.  
 XX PD 10-APR-2001.  
 XX PF 30-SEP-1999; 99JP-00279566.  
 XX PR 30-SEP-1999; 99JP-00279566.  
 XX PA (EGAW//) EGAWA K.  
 XX PA (MEDI-) MEDINET KK.  
 XX PA (KIMU//) KIMURA K.  
 XX DR WPI; 2001-360493/38.  
 XX DR N-PSDB; AAH45555.  
 XX PT Novel cancer cell-specific HLA-F antigen useful for diagnosing cancer.  
 XX PS Disclosure; Page 9-10; 12pp; Japanese.  
 XX CC This invention relates to a cancer cell specific HLA-F antigen. The  
 CC invention includes DNA encoding the antigen, and a method for the  
 CC preparation of the cancer cell specific HLA-F antigen. The antigen may be  
 CC used in a method to diagnose cancer, in which the protein is used to  
 CC detect anti-HLA-F antibodies in bodily fluids of the patient. The present  
 CC sequence represents the cancer cell-specific HLA-F antigen of the  
 CC invention  
 XX SQ Sequence 362 AA;  
 Query Match 100.0%; Score 274; DB 4; Length 362;  
 Best Local Similarity 100.0%; Pred. No. 6.6e-250;  
 Matches 274; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GSHSLRYSTAVSRGPRGEPYIAVEYVDDTQFLRFDSDAAIPRMEPRPWEQGPQYW 60  
 Db 22 GSHSLRYSTAVSRGPRGEPYIAVEYVDDTQFLRFDSDAAIPRMEPRPWEQGPQYW 81  
 QY 61 EWTGAKANAQTRVALRNLRRYNQSEAGSHTLQGMNGCDMPDGRLLRGYHQHAYDG 120

Db 82 EWTGAKANAQTRVALRNLRRYNQSEAGSHTLQGMNGCDMPDGRLLRGYHQHAYDG 141  
 QY 121 KDYISLNEDLSRWTAAADTVAQITQRFYEAEBEYAEFFTYLEGECLLELLRRYLENGKETLQ 180  
 Db 142 KDYISLNEDLSRWTAAADTVAQITQRFYEAEBEYAEFFTYLEGECLLELLRRYLENGKETLQ 201  
 QY 181 RADPPKHAHVHPISDHEATLRCWALGFYPAEITLTWQRDGEQCTODTELVEVTRPAGDGT 240  
 Db 202 RADPPKHAHVHPISDHEATLRCWALGFYPAEITLTWQRDGEQCTODTELVEVTRPAGDGT 261  
 QY 241 FQKWAADVVPSEGEQRYTCHVQHEGLPOPLILRW 274  
 Db 262 FQKWAADVVPSEGEQRYTCHVQHEGLPOPLILRW 295  
 RESULT 3  
 ABB50296  
 ID ABB50296 standard; protein; 362 AA.  
 XX AC ABB50296;  
 XX DT 08-FEB-2002 (first entry)  
 XX DE HLA-Cw ovarian tumour marker protein, SEQ ID NO:82.  
 XX KW Ovarian tumour marker gene; human; overexpression; upregulation;  
 KW epithelial tumour; cancer; diagnosis; prognosis; disease monitoring;  
 KW identification; serous cystadenoma; borderline serous tumour;  
 KW serous cystadenocarcinoma; mucinous mucinous tumour; endometrioid carcinoma;  
 KW undifferentiated carcinoma; clear cell adenocarcinoma; cystadenofibroma;  
 KW adenofibroma; Brenner tumour; serial analysis of gene expression; SAGE;  
 KW immune response pathway; cell proliferation regulation; protein folding;  
 KW membrane localised; secreted; therapeutic target; cytostatic;  
 KW gene therapy; vaccine.  
 XX OS Homo sapiens.  
 XX WO200175177-A2.  
 XX PD 11-OCT-2001.  
 XX PF 03-APR-2001; 2001WO-US010947.  
 XX PR 03-APR-2000; 2000US-0194336P.  
 XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 XX PI Morin PJ, Sherman-Baust CA, Pizer ES, Hough CD;  
 XX WPI; 2001-626450/72.  
 XX DR N-PSDB; ABA83122.  
 XX PT Detecting and identifying ovarian tumor, identifying increased risk for  
 PT developing ovarian cancer, and determining effectiveness of ovarian  
 PT cancer treatment, by measuring expression level of ovarian tumor marker  
 PT gene.  
 XX PS Claim 23; Page 126-127; 140pp; English.  
 XX CC The invention relates to methods for diagnosing and prognosing ovarian  
 CC tumours in an individual via the detection and measurement of the  
 CC expression of ovarian tumour marker genes (ABA831081-ABA83122, ABA83180,  
 CC ABA83182 and ABA83184) or segments thereof (ABA83123-ABA83169, ABA83179,  
 CC ABA83181 and ABA83183). The methods of the invention are useful for  
 CC detecting an ovarian tumour in a patient, for identifying an individual  
 CC at increased risk for developing ovarian cancer, in prognostic tests for  
 CC assessing the relative severity of ovarian cancer, in tests for  
 CC monitoring a patient in remission from ovarian cancer and in tests for  
 CC monitoring disease status in a patient being treated for ovarian cancer.  
 CC The methods can additionally be used to identify a particular tumour as  
 CC being an ovarian tumour (i.e., an epithelial ovarian tumour selected from  
 CC serous cystadenoma, borderline serous tumour, serous cystadenocarcinoma,

CC mucinous cystadenoma, borderline mucinous tumour, mucinous  
CC cystadenocarcinoma, endometrioid carcinoma, undifferentiated carcinoma,  
CC clear cell adenocarcinoma, cystadenofibroma, adenofibroma and Brenner  
CC tumour. The ovarian tumour marker genes of the invention were identified  
CC using SAGE (serial analysis of gene expression) and were found to be  
CC overexpressed in a broad variety of ovarian epithelial tumour cells  
CC relative to normal ovarian epithelial cells. The marker genes are  
CC implicated in immune response pathways, in the regulation of cell  
CC proliferation and in protein folding, and many of these are membrane-  
CC localised or secreted. In addition to their use as diagnostic and  
CC prognostic markers, the ovarian tumour marker genes or their encoded  
CC proteins may be used as therapeutic targets for the treatment and  
CC prevention of ovarian cancer. Sequences ABB50257-ABB50299 represent  
CC proteins encoded by ovarian tumour marker genes of the invention  
XX  
SQ Sequence 362 AA;  
  
Query Match 100.0%; Score 274; DB 4; Length 362;  
Best Local Similarity 100.0%; Pred. No. 6.6e-250;  
Matches 274; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 GSHSLRYFSTAVSRPGEGEPRYIAVEYVDDTQFLRFDSDAI PRMEPREPWEQGPQYW 60  
Db 22 GSHSLRYFSTAVSRPGEGEPRYIAVEYVDDTQFLRFDSDAI PRMEPREPWEQGPQYW 81  
  
Qy 61 EWTTCYAKANAQTDRAVALNLLRRYNOSEAGSHTLQGMNGCDMGDPDGLRLRGYHQHAYDG 120  
Db 82 EWTTCYAKANAQTDRAVALNLLRRYNOSEAGSHTLQGMNGCDMGDPDGLRLRGYHQHAYDG 141  
  
Qy 121 KDYISLNEEDLSRWSAATVAQITQRFYEAEYAEFPRTYLEGECLELLRRYLENGKETLQ 180  
Db 142 KDYISLNEEDLSRWSAATVAQITQRFYEAEYAEFPRTYLEGECLELLRRYLENGKETLQ 201  
  
Qy 161 RADPPKARVAHPISDHEATLRCAWALGFYPAEITLTWQDGEQOTDELVELTRPAGDGT 240  
Db 202 RADPPKARVAHPISDHEATLRCAWALGFYPAEITLTWQDGEQOTDELVELTRPAGDGT 261  
  
Qy 241 FQKWAAVVPSGEEQRYTCHVQHEGLPQLILRW 274  
Db 262 FQKWAAVVPSGEEQRYTCHVQHEGLPQLILRW 295  
  
RESULT 4  
ABG26726  
ID ABG26726 standard; protein; 677 AA.  
XX  
AC ABG26726;  
XX  
DT 18-FEB-2002 (first entry)  
XX  
DE Novel human diagnostic protein #26717.  
XX  
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;  
KW food supplement; medical imaging; diagnostic; genetic disorder.  
XX  
OS Homo sapiens.  
XX  
PN WO200175067-A2.  
XX  
PD 11-OCT-2001.  
XX  
PF 30-MAR-2001; 2001WO-US008631.  
XX  
PR 31-MAR-2000; 2000US-00540217.  
PR 23-AUG-2000; 2000US-00649167.  
XX  
PA (HYSE-) HYSEQ INC.  
XX  
PI Drmanac RT, Liu C, Tang YT;  
XX  
DR WPI; 2001-639362/73.  
DR N-PSDB; AAG90913.  
XX

PT New isolated polynucleotide and encoded polypeptides, useful in  
PT diagnostics, forensics, gene mapping, identification of mutations  
PT responsible for genetic disorders or other traits and to assess  
PT biodiversity.  
XX  
PS Claim 20; SEQ ID NO 57085; 103bp; English.  
XX  
CC The invention relates to isolated polynucleotide (I) and polypeptide (II)  
CC sequences. (I) is useful as hybridisation probes, polymerase chain  
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,  
CC and in recombinant production of (II). The polynucleotides are also used  
CC in diagnostics as expressed sequence tags for identifying expressed  
CC genes. (I) is useful in gene therapy techniques to restore normal  
CC activity of (II) or to treat disease states involving (II). (II) is  
CC useful for generating antibodies against it, detecting or quantitating a  
CC polypeptide in tissue, as molecular weight markers and as a food  
CC supplement. (II) and its binding partners are useful in medical imaging  
CC of sites expressing (II). (I) and (II) are useful for treating disorders  
CC involving aberrant protein expression or biological activity. The  
CC polypeptide and polynucleotide sequences have applications in  
CC diagnostics, forensics, gene mapping, identification of mutations  
CC responsible for genetic disorders or other traits to assess biodiversity  
CC and to produce other types of data and products dependent on DNA and  
CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic  
CC amino acid sequences of the invention. Note: The sequence data for this  
CC patent did not appear in the printed specification, but was obtained in  
CC electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 677 AA;  
  
Query Match 91.2%; Score 250; DB 4; Length 677;  
Best Local Similarity 100.0%; Pred. No. 4.7e-227;  
Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 GSHSLRYFSTAVSRPGEGEPRYIAVEYVDDTQFLRFDSDAI PRMEPREPWEQGPQYW 60  
Db 331 GSHSLRYFSTAVSRPGEGEPRYIAVEYVDDTQFLRFDSDAI PRMEPREPWEQGPQYW 390  
  
Qy 61 EWTTCYAKANAQTDRAVALNLLRRYNOSEAGSHTLQGMNGCDMGDPDGLRLRGYHQHAYDG 120  
Db 391 EWTTCYAKANAQTDRAVALNLLRRYNOSEAGSHTLQGMNGCDMGDPDGLRLRGYHQHAYDG 450  
  
Qy 121 KDYISLNEEDLSRWSAATVAQITQRFYEAEYAEFPRTYLEGECLELLRRYLENGKETLQ 180  
Db 451 KDYISLNEEDLSRWSAATVAQITQRFYEAEYAEFPRTYLEGECLELLRRYLENGKETLQ 510  
  
Qy 181 RADPPKARVAHPISDHEATLRCAWALGFYPAEITLTWQDGEQOTDELVELTRPAGDGT 240  
Db 511 RADPPKARVAHPISDHEATLRCAWALGFYPAEITLTWQDGEQOTDELVELTRPAGDGT 570  
  
Qy 241 FQKWAAVVVP 250  
Db 571 FQKWAAVVVP 580  
  
RESULT 5  
AAB43986  
ID AAB43986 standard; protein; 271 AA.  
XX  
AC AAB43986;  
XX  
DT 08-FEB-2001 (first entry)  
XX  
DE Human cancer associated protein sequence SEQ ID NO:1431.  
XX  
KW Human; cancer associated gene; cancer antigen; detection; cancer;  
KW diagnoses; cytostatic; proliferative; vulvar; immunomodulator;  
KW antidiabetic; antistatic; antirheumatic; antithrombotic; antiviral;  
KW antiinflammatory; antichryoid; antiallergic; antibacterial; cardiant;  
KW dermatologic; neuroprotective; thrombolytic; coagulant; nootropic;  
KW vasotropic; antipsoriatic; antiangiogenic; gene therapy; inflammation;  
KW immune disorder; haematopoietic cell disorder; autoimmune disorder;  
KW

KW allergic reaction; graft versus host disease; organ rejection;  
KW haemostatic; thrombolytic; cardiovascular disorder; infection;  
KW neurological disease; drug screening.

XX Homo sapiens.  
XX WO20005350-A1.  
XX 21-SEP-2000.  
XX 08-MAR-2000; 2000WO-US005882.  
XX 12-MAR-1999; 99US-0124270P.  
XX (HUMA-) HUMAN GENOME SCI INC.  
XX Rosen CA, Ruben SM;  
XX WPI; 2000-587533/55.  
XX N-PSDB; AAC78195.

XX Novel isolated nucleic acids comprising sequences encoding peptides  
XX useful for treating or diagnosing e.g. cancer.

XX Claim 11; Page 2115-2116; 2352pp; English.

XX AAC77607 to AAC78448 encode the human cancer associated proteins given in  
XX AAB43398 to AAB44239. The proteins can have activities based on the  
XX tissues and cells the genes are expressed in. Example of activities  
XX include: cytostatic; proliferative; vulnery; immunomodulator;  
XX antidiabetic; antiasthmatic; antirheumatic; antiarthritic;  
XX antiinflammatory; antithyroid; antiallergic; antibacterial; antiviral;  
XX dermatological; neuroprotective; cardiac; thrombolytic; coagulant;  
XX neotropic; vasotropic; antiporiatic and antiangiogenic. The  
XX polynucleotides and polypeptides can be used for preventing, treating or  
XX ameliorating medical conditions and diagnosing pathological conditions.  
XX Polynucleotides, polypeptides, antibodies, agonists and antagonists from  
XX the present invention may be used to treat immune disorders by activating  
XX or inhibiting the proliferation, differentiation or mobilisation of  
XX immune cells, to treat disorders of haematopoietic cells, autoimmune  
XX disorders, allergic reactions, graft versus host disease and organ  
XX rejection, modulate haemostatic or thrombolytic activity, modulate  
XX inflammation, cancers, cardiovascular disorders, neurological disease and  
XX bacterial or viral infections. The peptides, nucleotides, antibodies,  
XX agonists and antagonists may be also be used in drug screens. AAC78449 to  
XX AAC78457 and AAB44240 represent sequences used in the exemplification of  
XX the present invention

XX Sequence 271 AA;

Query Match 88.0%; Score 241; DB 3; Length 271;  
Best Local Similarity 100.0%; Pred. No. 7.1e-219;  
Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GSHSLRPFSTAVSRPGRGEPIYIAVEYVDDTQFLRFSDAAIPRMEPREPWVEGPGQYW 60  
Db 28 GSHSLRPFSTAVSRPGRGEPIYIAVEYVDDTQFLRFSDAAIPRMEPREPWVEGPGQYW 87  
QY 61 EWTGYAKANAQTRVALRNLLRRYNQSEAGSHTLQGMNGCDMGPDGRLRGYHCHAYDG 120  
Db 88 EWTGYAKANAQTRVALRNLLRRYNQSEAGSHTLQGMNGCDMGPDGRLRGYHCHAYDG 147  
QY 121 KDYISLNEDLSRSTAADTVAQITQRFYEAEBYAEFFRYLEGECLELLRRYLENGKETLQ 180  
Db 148 KDYISLNEDLSRSTAADTVAQITQRFYEAEBYAEFFRYLEGECLELLRRYLENGKETLQ 207  
QY 181 RADPPKAHVHPIPSDHEATLRCAWALGFYPAEITLTWQDGEEOQTDELVELVETRPAGDT 240  
Db 208 RADPPKAHVHPIPSDHEATLRCAWALGFYPAEITLTWQDGEEOQTDELVELVETRPAGDT 267  
QY 241 F 241  
Db 268 F 268

RESULT 6  
AAG64619

ID AAG64619 standard; protein; 215 AA.

XX AAG64619;

AC AAG64619;

XX 12-SEP-2001 (first entry)

XX Human cancer cell specific HLA-F antigen SEQ ID 6.

XX HLA-F antigen; cancer cell specific; human.

XX Homo sapiens.

XX JP2001095584-A.

XX 10-APR-2001.

XX 30-SEP-1999; 99JP-00279566.

XX 30-SEP-1999; 99JP-00279566.

XX (EGAW/) EGAWA K.

XX (MEDI-) MEDINET KK.

XX (KIMU/) KIMURA K.

XX WPI; 2001-360493/38.

XX N-PSDB; AAH45557.

XX Novel cancer cell-specific HLA-F antigen useful for diagnosing cancer.

XX Claim 1; Page 11-12; 12pp; Japanese.

XX This invention relates to a cancer cell specific HLA-F antigen. The  
XX invention includes DNA encoding the antigen, and a method for the  
XX preparation of the cancer cell specific HLA-F antigen. The antigen may be  
XX used in a method to diagnose cancer, in which the protein is used to  
XX detect anti-HLA-F antibodies in bodily fluids of the patient. The present  
XX sequence represents the cancer cell-specific HLA-F antigen of the  
XX invention

XX Sequence 215 AA;

Query Match 78.5%; Score 215; DB 4; Length 215;  
Best Local Similarity 100.0%; Pred. No. 2e-194;  
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 IAVEYVDDTQFLRFSDAAIPRMEPREPWVEGPGQYWEWTTGYAKANAQTRVALRNLL 82

Db 1 IAVEYVDDTQFLRFSDAAIPRMEPREPWVEGPGQYWEWTTGYAKANAQTRVALRNLL 60

QY 83 RRYNQEAGSHTLQGMNGCDMGPDGRLRGYHCHAYDGKDYISLNEDLSRSTAADTVAQI 142

Db 61 RRYNQEAGSHTLQGMNGCDMGPDGRLRGYHCHAYDGKDYISLNEDLSRSTAADTVAQI 120

QY 143 TQRFYEAEBYAEFFRYLEGECLELLRRYLENGKETLQADPPKAHVHPIPSDHEATLR 202

Db 121 TQRFYEAEBYAEFFRYLEGECLELLRRYLENGKETLQADPPKAHVHPIPSDHEATLR 180

QY 203 CWALGFYPAEITLTWQDGEEOQTDELVELVETRPAG 237

Db 181 CWALGFYPAEITLTWQDGEEOQTDELVELVETRPAG 215

RESULT 7

AAG00209

ID AAG00209 standard; protein; 120 AA.

XX AAG00209;

XX 06-OCT-2000 (first entry)

XX Human secreted protein, SEQ ID NO: 4290.  
 XX Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;  
 KW Gene therapy; chromosome mapping.  
 XX Homo sapiens.  
 OS  
 XX EP1033401-A2.  
 PN  
 XX 06-SEP-2000.  
 PD  
 XX 21-FEB-2000; 2000EP-00200610.  
 PF  
 XX 26-FEB-1999; 99US-0122487P.  
 PR  
 XX (GEST ) GENSET.  
 PA  
 XX Dumas Milne Edwards J, Duclert A, Giordano J;  
 PI WPI; 2000-500381/45.  
 XX N-PSDB; AAC00215.  
 DR  
 XX New nucleic acid that is a 5' expressed sequence tag (5' EST) for  
 PT obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for  
 PT diagnostic, forensic, gene therapy and chromosome mapping procedures.  
 PT  
 XX Claim 13; SEQ ID NO 4290; 71pp + Sequence Listing; English.  
 PS  
 XX The present sequence is a polypeptide encoded by one of a large number of  
 CC 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were  
 CC prepared from total human RNAs or polyA+ RNAs derived from 30 different  
 CC tissues. EST sequences usually correspond mainly to the 3' untranslated  
 CC region (UTR) of the mRNA because they are often obtained from oligo-dT  
 CC primed cDNA libraries. Such ESTs are not well suited for isolating cDNA  
 CC sequences derived from the 5' ends of mRNAs and even in those cases where  
 CC longer cDNA sequences have been obtained, the full 5' UTR is rarely  
 CC included. 5' ESTs are derived from mRNAs with intact 5' ends and can  
 CC therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs  
 CC are also used in diagnostic, forensic, gene therapy and chromosome  
 CC mapping procedures. They are used to obtain upstream regulatory sequences  
 CC and to design expression and secretion vectors  
 XX  
 XX Sequence 120 AA;  
 SQ  
 Query Match 36.1%; Score 99; DB 3; Length 120;  
 Best Local Similarity 100.0%; Pred. No. 3.3e-85;  
 Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GSHSLYFSTAVSRGPGEPRIYAVYVDVDTQFLRFDSDAALPRMEPRPWPVEQSGPQYW 60  
 DB 22 GSHSLYFSTAVSRGPGEPRIYAVYVDVDTQFLRFDSDAALPRMEPRPWPVEQSGPQYW 81  
 QY 61 EMTTGYAKANAQTDRLVALNRLRLRYNQSGAGSHTLQGMN 99  
 DB 82 EMTTGYAKANAQTDRLVALNRLRLRYNQSGAGSHTLQGMN 120  
 RESULT 8  
 ABP42931  
 ID -ABP42931 standard; protein; 186 AA.  
 XX  
 AC ABP42931;  
 XX  
 XX 22-AUG-2002 (first entry)  
 DT  
 XX Human ovarian antigen HPDRT37, SEQ ID NO:4063.  
 DE  
 XX Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;  
 KW ovarian cancer; breast cancer; tumour; reproductive system disorder;  
 KW infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;  
 KW PCOS; ovarian cyst; dysmenorrhea; endocrine disorder; infection;  
 KW inflammatory condition; immune disorder; blood disorder;  
 KW

KW cardiovascular disorder; respiratory disorder; neurological disorder;  
 KW gastrointestinal disorder; urinary system disorder; drug screening;  
 KW gene therapy; chromosome mapping; forensic analysis;  
 KW antibody preparation; cytostatic; immunomodulatory; neuroprotective;  
 KW antiinflammatory; gynaecological; reproductive.  
 XX  
 OS Homo sapiens.  
 XX WO200200677-A1.  
 PN  
 XX 03-JAN-2002.  
 PD  
 XX 07-JUN-2001; 2001WO-US018569.  
 PF  
 XX 07-JUN-2000; 2000US-0209467P.  
 PR  
 XX (HUMA-) HUMAN GENOME SCI INC.  
 PA  
 XX Birse CE, Rosen CA;  
 PI WPI; 2002-147878/19.  
 XX N-PSDB; ABQ56008.  
 DR  
 XX Isolated nucleic acid molecules encoding novel ovarian polypeptides,  
 PT useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian  
 PT cancer), immune disorders, cardiovascular disorders and neurological  
 PT diseases.  
 PT  
 XX Claim 11; SEQ ID NO 4063; 2922pp; English.  
 PS  
 XX The invention relates to 2175 novel human ovarian antigens (ABP41054-  
 CC ABP43228) and to cDNAs encoding them (ABQ54131-ABQ56305), and also  
 CC encompasses polypeptides 90% identical and polynucleotides 95% identical  
 CC to the sequences of the invention. The invention additionally relates to  
 CC recombinant vectors and host cells comprising human ovarian antigen  
 CC polynucleotides, antibodies against human ovarian antigens, and the use  
 CC of ovarian antigen polynucleotides and polypeptides in diagnosing,  
 CC treating, prognosing or preventing various ovary and/or breast-related  
 CC disorders. Such conditions include ovarian cancer and breast cancer, and  
 CC metastatic tumours of ovarian or breast origin, reproductive system  
 CC disorders (e.g., infertility, disorders of pregnancy, anovulation,  
 CC polycystic ovary syndrome, ovarian cysts, and dysmenorrhea), endocrine  
 CC disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic  
 CC shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and  
 CC vaginitis), immune disorders (e.g., congenital and acquired  
 CC immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus),  
 CC blood-related disorders (e.g., anaemia), cardiovascular disorders,  
 CC respiratory disorders, neurological disorders, gastrointestinal disorders  
 CC and urinary system disorders. Ovarian antigen polypeptides and  
 CC polynucleotides may also be used in screening for compounds which  
 CC modulate ovarian antigen expression or activity. The polynucleotides may  
 CC further be used for gene therapy, chromosome mapping, in the  
 CC identification of individuals and in forensic analysis, and the  
 CC polypeptides may be used as food additives or to prepare antibodies  
 CC useful in disease diagnosis, drug targeting and phenotyping. The present  
 CC sequence represents a human ovarian antigen of the invention. Note: The  
 CC sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 186 AA;  
 Query Match 25.5%; Score 70; DB 5; Length 186;  
 Best Local Similarity 100.0%; Pred. No. 1e-57;  
 Matches 70; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 66 YAKANAQTDRLVALNRLRLRYNQSGAGSHTLQGMNCDMPGRLRLRGVHAYDKQYIS 125  
 DB 1 YAKANAQTDRLVALNRLRLRYNQSGAGSHTLQGMNCDMPGRLRLRGVHAYDKQYIS 60  
 QY 126 LNEDLRSWTA 135  
 DB 61 LNEDLRSWTA 70



AAAP80911 standard; protein; 274 AA.  
AAP80911;  
25-MAR-2003 (revised)  
18-SEP-1990 (first entry)  
Consensus sequence of peptides which constitute the alpha-1, alpha-2 and alpha-3 regions of a class I HLA molecule.  
HLA-A2 epitopes; extracellular domains alpha-1, alpha-2 and alpha-3.  
Homo sapiens.  
Key Location/Qualifiers  
Region 1..90 /note= "alpha-1 region"  
Region 91..180 /note= "alpha-2 region"  
Region 181..272 /note= "alpha-3 region"  
WO805784-A.  
11-AUG-1988.  
27-JAN-1988; 88WO-US000245.  
30-JAN-1987; 87US-0008846.  
24-DEC-1987; 87US-00138547.  
(STRD ) UNIV LELAND STANFORD JUNIOR.  
Krensky AM, Farham P, Clayberger C;  
WPI; 1988-235147/33.  
New peptide corresp. to major histocompatibility antigen regions - used for modulating cytotoxic T-lymphocyte activity in e.g. transplants or auto-immune diseases.  
Example 9; Fig 4; 60pp; English.  
The consensus sequence is derived from a total of 23 HLA-A,B,C sequences. The protein sequences in the three extracellular domains (alpha-1, alpha-2 and alpha-3) are shown. The example concerned the effect of peptides from different HLA-A2 epitopes on cytotoxicity of target cells by CTL of different specificities. (Updated on 25-MAR-2003 to correct PA field.) (Updated on 25-MAR-2003 to correct PA field.)  
Sequence 274 AA;  
Query Match 16.1%; Score 44; DB 1; Length 274;  
Best Local Similarity 100.0%; Pred. No. 4.8e-33;  
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 224 QTQDTLVETRPAGDGTFOKAAVVVPSGEEQRYTCHVQHEGLP 267  
DB 224 QTQDTLVETRPAGDGTFOKAAVVVPSGEEQRYTCHVQHEGLP 267  
RESULT 11  
AAR12466  
ID AAR12466 standard; protein; 366 AA.  
XX AAR12466;  
AC AAR12466;  
XX 25-MAR-2003 (revised)  
DT 29-AUG-1991 (first entry)  
XX HLA-C exon Cb-2.  
XX

AAAB58497 standard; protein; 104 AA.  
AAB58497;  
14-MAR-2001 (first entry)  
Lung cancer associated polypeptide sequence SEQ ID 835.  
Human; lung cancer associated protein; neuroprotective; cytosolic; cardioactive; immunomodulatory; muscular active; vulnery; gastrointestinal; nephrotropic; antiinfective; gynecological; antibacterial; diagnosis; neural disorder; immune disorder; reproductive; proliferative disorder; wound healing; infectious disease.  
Homo sapiens.  
WO2000055180-A2.  
21-SEP-2000.  
08-MAR-2000; 2000WO-US005918.  
12-MAR-1999; 99US-0124270P.  
(HUMA-) HUMAN GENOME SCI INC.  
(ROSE/) ROSEN C A.  
Ruben SM;  
WPI; 2000-587514/55.  
N-PSDB; AAF18373.  
Lung cancer associated gene sequences, referred to as lung cancer antigens, useful for treatment, prevention, and diagnosis of disorders such as lung cancer.  
Claim 11; Page 1375; 1425pp; English.  
Polynucleotide sequences AAF17982 - AAF18424 encode human lung cancer associated proteins represented in AAB58106 - AAB58548. Lung cancer associated proteins and polynucleotide sequences, their agonists, and antagonists may have neuroprotective; cytosolic; cardioactive; immunomodulatory; muscular active general; vulnery; gastrointestinal general; nephrotropic; antiinfective; gynecological; or antibacterial activity. The invention also includes antibodies specific for the protein or polynucleotide sequences. The lung cancer associated polynucleotide sequences may be used for detection of lung cancer, chromosome identification, as chromosome markers, and for numerous other diagnostic or research purposes. The proteins may be used to treat disorders such as neural, immune, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal, and proliferative disorders. The proteins may also be used in the treatment of wounds and infectious diseases. Polynucleotide sequences AAF18425 - AAF18433 and peptide AAB58549 are used in the course of the invention for the identification and characterisation of the polynucleotide and protein sequences  
Sequence 104 AA;  
Query Match 16.1%; Score 44; DB 3; Length 104;  
Best Local Similarity 100.0%; Pred. No. 2.2e-33;  
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 224 QTQDTLVETRPAGDGTFOKAAVVVPSGEEQRYTCHVQHEGLP 267  
DB 32 QTQDTLVETRPAGDGTFOKAAVVVPSGEEQRYTCHVQHEGLP 75  
RESULT 10  
AAP80911

KW Human leukocyte antigen; probe; major histocompatibility complex; MHC;  
KW class I.  
XX Homo sapiens.  
XX JPO3112485-A.  
XX PD 14-MAY-1991.  
XX 22-SEP-1989; 89JP-00247695.  
XX PR 22-SEP-1989; 89JP-00247695.  
XX PA (OLYU ) OLYMPUS OPTICAL CO LTD.  
XX WPI; 1991-182989/25.  
XX DR N-PSDB; AAQ12117.  
XX HLA-C gene, DNA probe and transformant cells - for immunisation of  
PT animals and monoclonal antibody development.  
XX Claim 4; Page 2; 13pp; Japanese.  
XX Probes comprising part of the DNA sequence encoding the protein can be  
CC used to identify Class I genes. The DNA can be expressed for immunisation  
CC of animals and prodn. of monoclonal antibodies specific for the HLA-C  
CC antigen. See also AAPI2465 (same patent) and J03112486 and J03112487.  
CC (Updated on 25-MAR-2003 to correct PA field.)  
XX SQ Sequence 366 AA;  
Query Match 16.1%; Score 44; DB 2; Length 366;  
Best Local Similarity 100.0%; Pred. No. 6e-33;  
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 224 QTQDTLVETRPAGDGTFOKWAAVVPSGGEQRYTCHVQHEGLP 267  
Db 248 QTQDTLVETRPAGDGTFOKWAAVVPSGGEQRYTCHVQHEGLP 291  
RESULT 12  
AAV07033  
ID AAY07033 standard; protein; 366 AA.  
AC AAY07033;  
XX 02-JUL-1999 (first entry)  
DE Breast cancer associated antigen precursor sequence.  
XX Cancer associated antigen; diagnosis; research; treatment; human;  
KW breast cancer; colon cancer; gastric cancer; renal cancer; lung cancer;  
KW prostate cancer.  
XX Homo sapiens.  
XX WO9904265-A2.  
XX 28-JAN-1999.  
XX 15-JUL-1998; 98WO-US014679.  
XX 17-JUL-1997; 97US-00896164.  
XX 10-OCT-1997; 97US-0061599P.  
XX 10-OCT-1997; 97US-0061765P.  
XX 10-OCT-1997; 97US-00948705.  
XX 11-OCT-1997; 97GB-00021697.  
XX 22-JUN-1998; 98US-0010322.  
XX (LUDW-) LUDWIG INST CANCER RES.  
XX Old LJ, Scanlan MJ, Stockert E, Gure A, Chen Y, Gout I;  
PI O'hare M, Obata Y, Pfreundschuh M, Tureci O, Sahin U;

XX WPI; 1999-132448/11.  
XX New isolated cancer associated nucleic acids and polypeptides - isolated  
PT using sera from cancer patients, used to develop products for the  
PT diagnosis, monitoring or treatment of cancers.  
XX PS Disclosure; Page 417-418; 787pp; English.  
XX The invention relates to a method for diagnosing a disorder characterised  
CC by expression of a human cancer associated antigen precursor coded for by  
CC a nucleic acid molecule (NAM). The method comprises: (a) contacting a  
CC biological sample isolated from a subject with an agent that specifically  
CC binds to the NAM, an expression product or a fragment of an expression  
CC product complexed with an HLA molecule; and (b) determining the  
CC interaction between the agent and the NAM or the expression product as a  
CC determination of the disorder. The products and methods can be used in  
CC the diagnosis, monitoring, research, or treatment of conditions  
CC characterised by the expression of various cancer associated antigens.  
CC The invention provides nucleic acid sequences and encoded polypeptides  
CC which are cancer associated antigen precursors expressed in human breast  
CC cancer, renal cancer, colon cancer, gastric cancer, prostate cancer and  
CC lung cancer  
XX SQ Sequence 366 AA;  
Query Match 16.1%; Score 44; DB 2; Length 366;  
Best Local Similarity 100.0%; Pred. No. 6e-33;  
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 224 QTQDTLVETRPAGDGTFOKWAAVVPSGGEQRYTCHVQHEGLP 267  
Db 248 QTQDTLVETRPAGDGTFOKWAAVVPSGGEQRYTCHVQHEGLP 291  
RESULT 13  
AAO13073  
ID AAO13073 standard; protein; 374 AA.  
XX AAO13073;  
XX 06-NOV-2001 (first entry)  
XX Human polypeptide SEQ ID NO 26965.  
XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;  
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;  
KW tissue growth factor; immunomodulatory; cancer; leukaemia;  
KW nervous system disorders; arthritis; inflammation.  
XX Homo sapiens.  
XX WO200164835-A2.  
XX 07-SEP-2001.  
XX 26-FEB-2001; 2001WO-US004927.  
XX 28-FEB-2000; 2000US-00515126.  
XX 18-MAY-2000; 2000US-00577409.  
XX (HYSE-) HYSEQ INC.  
XX Tang YT, Liu C, Drmanac RT;  
XX WPI; 2001-514838/56.  
XX N-PSDB; AA193004.  
XX Isolated nucleic acids and polypeptides, useful for preventing diagnosing  
PT and treating e.g. leukemia, inflammation and immune disorders.  
XX Claim 20; SEQ ID NO 26965; 1399pp + Sequence Listing; English.

CC The invention relates to human polynucleotides (AA179941-AA193841) and  
CC the encoded proteins (AA00010-AA013910) that exhibit activity relating to  
CC cytokine, cell proliferation or cell differentiation or which may induce  
CC production of other cytokines in other cell populations. The  
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or  
CC peptide therapy. The polypeptides have various cytokine-like activities,  
CC e.g. stem cell growth factor activity, haematopoiesis regulating  
CC activity, tissue growth factor activity, immunomodulatory activity and  
CC activin/inhibin activity and may be useful in the diagnosis and/or  
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and  
CC inflammation. Note: The sequence data for this patent did not form part  
CC of the printed specification, but was obtained in electronic format  
CC directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
XX  
SQ Sequence 374 AA;

Query Match 16.1%; Score 44; DB 4; Length 374;  
Best Local Similarity 100.0%; Pred. No. 6.1e-33;  
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 224 QTQDTVELVETRPAGDGTFOKWAAVVPSGEEQRYTCHVQHEGLP 267  
Db 256 QTQDTVELVETRPAGDGTFOKWAAVVPSGEEQRYTCHVQHEGLP 299

## RESULT 14

AAU32883  
ID AAU32883 standard; protein; 380 AA.

XX AAU32883;

DT 18-DEC-2001 (first entry)

XX Novel human secreted protein #3374.

XX Human; vaccination; Gene therapy; nutritional supplement;  
XX stem cell proliferation; haematopoiesis; nerve tissue regeneration;  
XX immune suppression; immune stimulation; anti-inflammatory; leukaemia.

OS Homo sapiens.

XX WO200179449-A2.

XX 25-OCT-2001.

XX 16-APR-2001; 2001WO-US0008656.

XX 18-APR-2000; 2000US-00552929.

XX 26-JAN-2001; 2001US-00770160.

XX (HYSE-) HYSEQ INC.

XX Tang YT, Liu C, Drmanac RT;

XX WPI; 2001-611725/70.

XX Nucleic acids encoding a range of human polypeptides, useful in genetic  
XX vaccination, testing and therapy.

XX Claim 20; Page 683-684; 765pp; English.

XX The invention relates to novel human secreted polypeptides. The  
XX polypeptides and antibodies to the polypeptides are useful for  
XX determining the presence of or predisposition to a disease associated  
XX with altered levels of polypeptide. The polypeptides are also useful for  
XX identifying agents (agonists and antagonists) that bind to them. Cells  
XX expressing the proteins are useful for identifying a therapeutic agent  
XX for use in treatment of a pathology related to aberrant expression or  
XX physiological interactions of the polypeptide. Vectors comprising the  
XX nucleic acids encoding the polypeptides and cells genetically engineered  
XX to express them are also useful for producing the proteins. The proteins  
XX are useful in genetic vaccination, testing and therapy, and can be used  
XX as nutritional supplements. They may be used to increase stem cell

CC proliferation; to regulate haematopoiesis; and in bone, cartilage, tendon  
CC and/or nerve tissue growth or regeneration; immune suppression and/or  
CC stimulation; as anti-inflammatory agents; and in treatment of leukaemias.  
CC AAU9510-AAU3304 represent the amino acid sequences of novel human  
XX secreted proteins of the invention

SQ Sequence 380 AA;

Query Match 16.1%; Score 44; DB 4; Length 380;  
Best Local Similarity 100.0%; Pred. No. 6.2e-33;  
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 224 QTQDTVELVETRPAGDGTFOKWAAVVPSGEEQRYTCHVQHEGLP 267  
Db 256 QTQDTVELVETRPAGDGTFOKWAAVVPSGEEQRYTCHVQHEGLP 299

## RESULT 15

AAE90793

ID AAE90793 standard; protein; 120 AA.

XX AAE90793;

DT 15-JUN-2001 (first entry)

XX Human shear stress-response protein SEQ ID NO: 86.

XX Human; shear stress-response protein; vascular disease; arteriosclerosis.

OS Homo sapiens.

XX WO200125427-A1.

XX 12-APR-2001.

XX 02-OCT-2000; 2000WO-JP006840.

XX 01-OCT-1999; 99JP-00280976.

XX (KYOW) KYOWA HAKKO KOGYO KK.

XX (NOJI) NOJIMA H.

XX Nojima H, Yoshisue H, Obayashi M, Ota T, Kawabata A, Sakurada K;

XX Kuga T, Sekine S, Nakamura Y, Sugano S;

XX WPI; 2001-266308/27.

XX N-PSDB; AAH02916.

XX DNA sequences, proteins encoded by them and antibodies against them  
XX useful in diagnosis and treatment of vascular disease caused by  
XX arteriosclerosis.

XX Claim 60; Page 471-472; 678pp; Japanese.

XX The present invention provides the protein and coding sequences of a  
XX number of human shear stress response proteins. These are useful in the  
XX diagnosis, treatment and screening of vascular diseases caused by  
XX arteriosclerosis, including heart failure, post-PTCA restenosis and  
XX hypertension

SQ Sequence 120 AA;

Query Match 15.7%; Score 43; DB 4; Length 120;  
Best Local Similarity 100.0%; Pred. No. 2.2e-32;  
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 225 TQDTVELVETRPAGDGTFOKWAAVVPSGEEQRYTCHVQHEGLP 267

Db 8 TQDTVELVETRPAGDGTFOKWAAVVPSGEEQRYTCHVQHEGLP 50

Search completed: June 18, 2004, 19:29:54

Job time : 63 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 18, 2004, 19:27:12 ; Search time 45 Seconds  
(without alignments)  
1921.155 Million cell updates/sec

Title: US-09-819-371-5

Perfect score: 274

Sequence: 1 GSHSLRYSTAVSRGRGEP.....QRYTCHVQHEGLPQLILRW 274

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 1017041 seqs, 315518202 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

SPTREMBL 25:  
1: sp\_archaea:  
2: sp\_bacteria:  
3: sp\_fungi:  
4: sp\_human:  
5: sp\_invertebrate:  
6: sp\_mammal:  
7: sp\_mhc:  
8: sp\_organelle:  
9: sp\_phase:  
10: sp\_plant:  
11: sp\_rodent:  
12: sp\_virus:  
13: sp\_vertebrate:  
14: sp\_unclassified:  
15: sp\_virus:  
16: sp\_bacteriaph:  
17: sp\_archaeap:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	274	100.0	324	7 Q861F0	Q861F0 homo sapien
2	274	100.0	324	7 Q861E9	Q861E9 homo sapien
3	274	100.0	346	7 Q8WLP5	Q8WLP5 homo sapien
4	274	100.0	442	7 Q95HC0	Q95HC0 homo sapien
5	250	91.2	346	7 Q8MGQ1	Q8MGQ1 homo sapien
6	250	91.2	362	7 Q9TP68	Q9TP68 homo sapien
7	208	75.9	346	7 Q95IT2	Q95IT2 pan troglod
8	208	75.9	362	6 Q7YR27	Q7YR27 pan troglod
9	182	66.4	254	7 Q860R0	Q860R0 homo sapien
10	87	31.8	91	7 Q9TXX7	Q9TXX7 sorilla gor
11	73	26.6	316	7 Q29958	Q29958 homo sapien
12	62	22.6	314	7 Q860F6	Q860F6 macaca neme
13	61	22.3	353	7 Q9MXS7	Q9MXS7 macaca mula
14	61	22.3	353	7 Q9MXS6	Q9MXS6 macaca mula
15	61	22.3	365	7 Q9MXS5	Q9MXS5 macaca mula
16	59	21.5	59	7 Q78094	Q78094 homo sapien

17	45	16.4	330	7	Q30713	Q30713 macaca mula
18	45	16.4	338	7	Q95510	Q95510 leopardus p
19	45	16.4	359	7	Q30711	Q30711 macaca mula
20	44	16.1	91	7	Q9MY12	Q9MY12 homo sapien
21	44	16.1	91	7	Q9MY10	Q9MY10 homo sapien
22	44	16.1	91	7	Q9MYH8	Q9MYH8 homo sapien
23	44	16.1	91	7	Q7YF25	Q7YF25 homo sapien
24	44	16.1	91	7	Q7YNY6	Q7YNY6 homo sapien
25	44	16.1	91	7	Q7YNY3	Q7YNY3 homo sapien
26	44	16.1	259	7	Q29645	Q29645 homo sapien
27	44	16.1	273	7	Q9GIP0	Q9GIP0 homo sapien
28	44	16.1	273	7	Q9BCN8	Q9BCN8 homo sapien
29	44	16.1	273	7	Q8SNC6	Q8SNC6 homo sapien
30	44	16.1	273	7	Q8MGZ8	Q8MGZ8 homo sapien
31	44	16.1	273	7	Q9TQP8	Q9TQP8 homo sapien
32	44	16.1	273	7	Q8HWT0	Q8HWT0 homo sapien
33	44	16.1	273	7	Q95IG6	Q95IG6 homo sapien
34	44	16.1	298	7	Q29866	Q29866 homo sapien
35	44	16.1	298	7	Q79497	Q79497 homo sapien
36	44	16.1	298	7	Q19657	Q19657 homo sapien
37	44	16.1	298	7	Q19653	Q19653 homo sapien
38	44	16.1	298	7	Q19655	Q19655 homo sapien
39	44	16.1	312	7	Q860B5	Q860B5 homo sapien
40	44	16.1	312	7	Q860B4	Q860B4 homo sapien
41	44	16.1	313	7	Q30989	Q30989 pan troglod
42	44	16.1	313	7	Q9MY41	Q9MY41 homo sapien
43	44	16.1	314	7	Q860G9	Q860G9 macaca neme
44	44	16.1	318	7	Q7YFW4	Q7YFW4 homo sapien
45	44	16.1	319	7	Q861B7	Q861B7 homo sapien

#### ALIGNMENTS

#### RESULT 1

Q861F0 PRELIMINARY; PRT; 324 AA.  
ID Q861F0  
AC Q861F0; 24, Created  
DT 01-JUN-2003 (Tremblrel. 24, Last sequence update)  
DT 01-JUN-2003 (Tremblrel. 24, Last sequence update)  
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)  
DE Nonclassical MHC class I antigen (Fragment).  
GN HLA-F.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA He X., Xu L., Liu Y., Zeng Y.;  
RT "Nonclassical MHC class I HLA-F";  
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY216682; AAC37689.1;  
DR GO; GO:0016020; C:membrane; IEA.  
DR GO; GO:0006955; P:immune response; IEA.  
DR InterPro; IPR001064; Crystallin.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig cl.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR001039; MHC\_I.  
DR Pfam; PF00047; Ig; 1.  
DR Pfam; PF00129; MHC\_I; 1.  
DR PRINTS; PR01638; MHCCLASSI.  
DR ProDom; PD000050; MHC\_I; 1.  
DR SMART; SM00407; Igc1; 1.  
DR PROSITE; PS00225; CRYSTALLIN\_BETAGAMMA; 1.  
DR PROSITE; PS00835; IG\_LIKE; 1.  
DR PROSITE; PS00290; IG\_MHC; 1.  
FT NON TER 1 324  
FT NON TER 324 324  
SQ SEQUENCE 324 AA; 36518 MW; E3E028177D2716F4 CRC64;  
Query Match 100.0%; Score 274; DB 7; Length 324;

Best Local Similarity 100.0%; Pred. No. 3.1e-279; Matches 274; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSHSLRYSTAVSPRGGEPRYIAVEYVDDTQFLRFDSDAAIPRMEPREPWEQEGQYW 60  
 DB 18 GSHSLRYSTAVSPRGGEPRYIAVEYVDDTQFLRFDSDAAIPRMEPREPWEQEGQYW 77  
 QY 61 EWTGYAKANAQTDVALNLLRRYNQSEAGSHTLQNGMCDMGPDGRLLRGYHQHAYDG 120  
 DB 78 EWTGYAKANAQTDVALNLLRRYNQSEAGSHTLQNGMCDMGPDGRLLRGYHQHAYDG 137  
 QY 121 KDYSINEDLRSWTAADTVAQITQFYAEAEYAEAEFRVTEGECLELLRRYLENGKETLQ 180  
 DB 138 KDYSINEDLRSWTAADTVAQITQFYAEAEYAEAEFRVTEGECLELLRRYLENGKETLQ 197  
 QY 181 RADPPKARVAHPISDHEATLRCWALGFYPAEITLTWQDGEEOQTDELVETRPAGDGT 240  
 DB 198 RADPPKARVAHPISDHEATLRCWALGFYPAEITLTWQDGEEOQTDELVETRPAGDGT 257  
 QY 241 FOKWAAVVPSGEGQRYTCHVQHEGLPQPLILRW 274  
 DB 258 FOKWAAVVPSGEGQRYTCHVQHEGLPQPLILRW 291

RESULT 2

Q86LE9 ID Q86LE9 PRELIMINARY; PRT; 324 AA.

AC Q86LE9;  
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE MHC class I antigen (Fragment).  
 GN HLA-F.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Liu Y., Xu L., Zeng Y., He X.;  
 RT "A new polymorphism in non-classical MHC class I HLA-F";  
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY221102; AA034407.1; -  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR GO; GO:0006955; P:immune response; IEA.  
 DR InterPro; IPR001064; Crystallin.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003597; IG.CI.  
 DR InterPro; IPR003006; IG.MHC.  
 DR InterPro; IPR001039; MHC\_I.  
 DR Pfam; PF00047; Ig.1.  
 DR Pfam; PF00129; MHC\_I.1.  
 DR PRINTS; PR01638; MHCCLASSI.  
 DR PRODOM; PD000050; MHC\_I.1.  
 DR SMART; SM00407; IGCL.1.  
 DR PROSITE; PS00225; CRYSTALLIN\_BETAGAMMA; 1.  
 DR PROSITE; PS00835; IG\_LIKE; 1.  
 DR PROSITE; PS00290; IG\_MHC; 1.  
 FT NON\_TER 1  
 FT NON\_TER 324 324  
 SQ SEQUENCE 324 AA; 36518 MW; E3E028177D2716F4 CRC64;

Query Match 100.0%; Score 274; DB 7; Length 324;  
 Best Local Similarity 100.0%; Pred. No. 3.1e-279; Matches 274; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSHSLRYSTAVSPRGGEPRYIAVEYVDDTQFLRFDSDAAIPRMEPREPWEQEGQYW 60  
 DB 18 GSHSLRYSTAVSPRGGEPRYIAVEYVDDTQFLRFDSDAAIPRMEPREPWEQEGQYW 77  
 QY 61 EWTGYAKANAQTDVALNLLRRYNQSEAGSHTLQNGMCDMGPDGRLLRGYHQHAYDG 120  
 DB 78 EWTGYAKANAQTDVALNLLRRYNQSEAGSHTLQNGMCDMGPDGRLLRGYHQHAYDG 137

QY 121 KDYSINEDLRSWTAADTVAQITQFYAEAEYAEAEFRVTEGECLELLRRYLENGKETLQ 180  
 DB 138 KDYSINEDLRSWTAADTVAQITQFYAEAEYAEAEFRVTEGECLELLRRYLENGKETLQ 197  
 QY 181 RADPPKARVAHPISDHEATLRCWALGFYPAEITLTWQDGEEOQTDELVETRPAGDGT 240  
 DB 198 RADPPKARVAHPISDHEATLRCWALGFYPAEITLTWQDGEEOQTDELVETRPAGDGT 257  
 QY 241 FOKWAAVVPSGEGQRYTCHVQHEGLPQPLILRW 274  
 DB 258 FOKWAAVVPSGEGQRYTCHVQHEGLPQPLILRW 291

RESULT 3

Q8WLP5 ID Q8WLP5 PRELIMINARY; PRT; 346 AA.

AC Q8WLP5;  
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE MHC class Ib antigen.  
 GN HLA-F.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Ishitani A., Miki A., Williams L.M., Moore Y., Geraghty D.E.;  
 RT "HLA-E, F, and G polymorphism: genomic sequence defines new variation spanning the nonclassical class I genes";  
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA He X., Liu Y., Xu L., Zeng Y.;  
 RT "Cloning of full-length HLA-F\*0101 variant 1 cDNA from Han Chinese";  
 RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA He X., Xu L., Liu Y., Zeng Y.;  
 RT "Cloning of full-length HLA-F\*0101 variant 2 cDNA from Han Chinese";  
 RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF523285; AAM74980.1; -  
 DR EMBL; AF523286; AAM74981.1; -  
 DR EMBL; AF523287; AAM74982.1; -  
 DR EMBL; AF523288; AAM74983.1; -  
 DR EMBL; AF523289; AAM74984.1; -  
 DR EMBL; AF523290; AAM74985.1; -  
 DR EMBL; AF523293; AAM74988.1; -  
 DR EMBL; AF523294; AAM74989.1; -  
 DR EMBL; AF523295; AAM74990.1; -  
 DR EMBL; AF523296; AAM74991.1; -  
 DR EMBL; AF523297; AAM74992.1; -  
 DR EMBL; AY253269; AAO86773.1; -  
 DR EMBL; AY253270; AAO86774.1; -  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR GO; GO:0006955; P:immune response; IEA.  
 DR InterPro; IPR001064; Crystallin.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003006; IG.MHC.  
 DR InterPro; IPR001039; MHC\_I.  
 DR Pfam; PF00047; Ig.1.  
 DR Pfam; PF00129; MHC\_I.1.  
 DR PRINTS; PR01638; MHCCLASSI.  
 DR PRODOM; PD000050; MHC\_I.1.  
 DR PROSITE; PS00225; CRYSTALLIN\_BETAGAMMA; 1.  
 DR PROSITE; PS00835; IG\_LIKE; 1.  
 DR PROSITE; PS00290; IG\_MHC; 1.  
 SQ SEQUENCE 346 AA; 39051 MW; D4782AA4697D57B2 CRC64;

Query Match 100.0%; Score 274; DB 7; Length 346;  
 Best Local Similarity 100.0%; Pred. No. 3.3e-279;



```
Db 202 RADPPKAVHHPISDHEATLRCWALGFYPAEITLTWQDGEQOTDELVETRPAGDGT 261
Qy 241 FQKAAVVVP 250
Db 262 FQKAAVVVP 271

RESULT 6
Q9TP68 PRELIMINARY; PRT; 362 AA.
AC Q9TP68 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE DJ37H14.9 (Major histocompatibility complex, class I, F
(CDA12)).
GN HLA-F.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Williams S.
AL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE
CC IMMUNE SYSTEM (BY SIMILARITY).
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN) (BY SIMILARITY).
DR EMBL; AL022723; CAB46623.1; -.
DR HSSP; Q30201; 146Z
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0006955; P: immune response; IEA.
DR InterPro; IPR001064; Crystallin.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR001039; MHC_I.
DR Pfam; PF00047; Ig; 1.
DR Pfam; PF00129; MHC_I; 1.
DR PRINTS; PR01638; MHCCLASSI.
DR ProDom; PD000050; MHC_I; 1.
DR SMART; SM00407; IGcl; 1.
DR PROSITE; PS00225; CRYSTALLIN BETAGAMMA; 1.
DR PROSITE; PS0835; IG LIKE; 1.
DR PROSITE; PS00290; IG_MHC; 1.
KW Glycoprotein; Transmembrane.
SQ SEQUENCE 362 AA; 40578 MW; 970D072C813A07E2 CRC64;

Query Match 91.2%; Score 250; DB 7; Length 362;
Best Local Similarity 100.0%; Pred. No. 5.9e-254;
Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GSHSLRYFSTAVSRPGRGEPYIAVEYVDDTQFLRFSDAAIPRMEPRPWPVEQGPQYW 60
Db 22 GSHSLRYFSTAVSRPGRGEPYIAVEYVDDTQFLRFSDAAIPRMEPRPWPVEQGPQYW 81
Qy 61 EWTGYAKANAQTRVALNRLRRYNQSEAGSHTLQGMNGCDMGPDGRLRGYHCHAYDG 120
Db 82 EWTGYAKANAQTRVALNRLRRYNQSEAGSHTLQGMNGCDMGPDGRLRGYHCHAYDG 141
Qy 121 KYISLNEDLSRSTAADTVAQITQRFYAEYAEFEFRYLEGECELELLRRYLENGKETLQ 180
Db 142 KYISLNEDLSRSTAADTVAQITQRFYAEYAEFEFRYLEGECELELLRRYLENGKETLQ 201
Qy 181 RADPPKAVHHPISDHEATLRCWALGFYPAEITLTWQDGEQOTDELVETRPAGDGT 240
Db 202 RADPPKAVHHPISDHEATLRCWALGFYPAEITLTWQDGEQOTDELVETRPAGDGT 261
Qy 241 FQKAAVVVP 250
Db 262 FQKAAVVVP 271

RESULT 7
Q95IT2 PRELIMINARY; PRT; 346 AA.
AC Q95IT2 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE MHC class I antigen.
GN PATR-F.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RA Adams E.J., Parham P.; PubMed=11398964;
RT "Genomic analysis of common chimpanzee major histocompatibility
complex class I genes.";
RL Immunogenetics 53:200-208 (2001).
DR EMBL; AF338355; AAK77479.1; -.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0006955; P: immune response; IEA.
DR InterPro; IPR001064; Crystallin.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR001039; MHC_I.
DR Pfam; PF00047; Ig; 1.
DR Pfam; PF00129; MHC_I; 1.
DR PRINTS; PR01638; MHCCLASSI.
DR ProDom; PD000050; MHC_I; 1.
DR SMART; SM00407; IGcl; 1.
DR PROSITE; PS00225; CRYSTALLIN BETAGAMMA; 1.
DR PROSITE; PS0835; IG LIKE; 1.
DR PROSITE; PS00290; IG_MHC; 1.
KW MHC.
SQ SEQUENCE 346 AA; 39009 MW; 0ECF12B7DB17B814 CRC64;

Query Match 75.9%; Score 208; DB 7; Length 346;
Best Local Similarity 100.0%; Pred. No. 8.1e-210;
Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 63 TTGYAKANAQTRVALNRLRRYNQSEAGSHTLQGMNGCDMGPDGRLRGYHCHAYDGKD 122
Db 84 TTGYAKANAQTRVALNRLRRYNQSEAGSHTLQGMNGCDMGPDGRLRGYHCHAYDGKD 143
Qy 123 YISLNEDLSRSTAADTVAQITQRFYAEYAEFEFRYLEGECELELLRRYLENGKETLQ 182
Db 144 YISLNEDLSRSTAADTVAQITQRFYAEYAEFEFRYLEGECELELLRRYLENGKETLQ 203
Qy 183 DPPKAVHHPISDHEATLRCWALGFYPAEITLTWQDGEQOTDELVETRPAGDGT 242
Db 204 DPPKAVHHPISDHEATLRCWALGFYPAEITLTWQDGEQOTDELVETRPAGDGT 263
Qy 243 KAAAVVVPSEGEQRYTCHVQHEGLPQL 270
Db 264 KAAAVVVPSEGEQRYTCHVQHEGLPQL 291

RESULT 8
Q7YR27 PRELIMINARY; PRT; 362 AA.
AC Q7YR27 (Tremblrel. 25, Created)
DT 01-OCT-2003 (Tremblrel. 25, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last sequence update)
DE Class IB.
GN PATR-F.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
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OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22709134; PubMed=12799463;
RA Yanagata T., Kuleki J.K., Naruse T.K., Fujimori Y., Fukuzumi Y.,
RA Yamagata T., Tashiro H., Iwamoto C., Umehara Y., Imanishi T.,
RA Meyer A., Ikeo K., Gojobori T., Bahram S., Inoko H.;
RT "Comparative sequencing of human and chimpanzee MHC class I regions
RT unveils insertions/deletions as the major path to genomic
RT divergence.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:7708-7713(2003).
SQ EMBL; AB100087; BAC78191.1; -.
SQ SEQUENCE 362 AA; 40625 MW; BAS699D08181A1FF CRC64;

Query Match 75.9%; Score 208; DB 6; Length 362;
Best Local Similarity 100.0%; Pred. No. 8.5e-210; Indels 0; Gaps 0;
Matches 208; Conservative 0; Mismatches 0;

QY 63 TTGYAKANAQTDRLVALNRLRRYNSGASHTLQMGNGCDMPDGRLLRGYHQHAYDGD 122
DB 84 TTGYAKANAQTDRLVALNRLRRYNSGASHTLQMGNGCDMPDGRLLRGYHQHAYDGD 143
QY 123 YISLNEDLSRSTAAADTVAQITQRYEAEYAEFEFTYLEGECLELLRRYLENGKETLQRA 182
DB 144 YISLNEDLSRSTAAADTVAQITQRYEAEYAEFEFTYLEGECLELLRRYLENGKETLQRA 203
QY 183 DPPKAVHHPISDHEATLRCWALGFYPAEITLTWQDGEQOTDELVETRPAGDGTQF 242
DB 204 DPPKAVHHPISDHEATLRCWALGFYPAEITLTWQDGEQOTDELVETRPAGDGTQF 263
QY 243 KWAAVVPSGEEQRYTCHVQHEGLPQPL 270
DB 264 KWAAVVPSGEEQRYTCHVQHEGLPQPL 291

RESULT 9
Q860R0 PRELIMINARY; PRT; 254 AA.
AC Q860R0;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE MHC class Ib antigen.
GN HLA-F.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX Liu Y., He X., Xu L., Zeng Y.;
RT "Cloning of full-length HLA-F*0101 variant 3 cDNA from Han Chinese.";
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY253271; AAC06775.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR001064; Cytoskeleton.
DR InterPro; IPR001039; MHC_I.
DR Pfam; PF00129; MHC_I.1.
DR PRINTS; PR01638; MHCCLASSI.
DR ProDom; PD000050; MHC_I.1.
DR PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; 1.
SQ SEQUENCE 254 AA; 28588 MW; C61F225D409AAED2 CRC64;

Query Match 66.4%; Score 182; DB 7; Length 254;
Best Local Similarity 100.0%; Pred. No. 1.3e-182; Indels 0; Gaps 0;
Matches 182; Conservative 0; Mismatches 0;

QY 1 GSHSLRFSTAVSPGEGEPRIYAVEVVDQTLRFDSDAALPRMEPRPWPVQEGPQYW 60
DB 22 GSHSLRFSTAVSPGEGEPRIYAVEVVDQTLRFDSDAALPRMEPRPWPVQEGPQYW 81
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QY 61 EWTGYAKANAQTDRLVALNRLRRYNSGASHTLQMGNGCDMPDGRLLRGYHQHAYDGD 120
DB 82 EWTGYAKANAQTDRLVALNRLRRYNSGASHTLQMGNGCDMPDGRLLRGYHQHAYDGD 141
QY 121 KDVISLNEDLSRSTAAADTVAQITQRYEAEYAEFEFTYLEGECLELLRRYLENGKETLQ 180
DB 142 KDVISLNEDLSRSTAAADTVAQITQRYEAEYAEFEFTYLEGECLELLRRYLENGKETLQ 201
QY 181 RA 182
DB 202 RA 203

RESULT 10
Q9TPX7 PRELIMINARY; PRT; 91 AA.
AC Q9TPX7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE MHC class I antigen (Fragment).
GN GOGO-F.
OS Gorilla gorilla (gorilla).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
OX NCBI_TaxID=9593;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Shamba;
RA Grimsley C.;
RT "HLA-F: A monomorphic locus in an African-American sample.";
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF159566; AAD51614.1; -.
DR InterPro; IPR007110; IG_Like.
DR InterPro; IPR003597; IG_C1.
DR InterPro; IPR003006; IG_MHC.
DR Pfam; PF00047; Ig; 1.
DR SMART; SMO0407; IGc1; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
DR PROSITE; PS00290; IG_MHC; 1.
DR NON_TER 1
FT NON_TER 91
SQ SEQUENCE 91 AA; 10354 MW; 2F485A66B6532A61 CRC64;

Query Match 31.8%; Score 87; DB 7; Length 91;
Best Local Similarity 100.0%; Pred. No. 3.9e-83; Indels 0; Gaps 0;
Matches 87; Conservative 0; Mismatches 0;

QY 184 PPKAVHHPISDHEATLRCWALGFYPAEITLTWQDGEQOTDELVETRPAGDGTQK 243
DB 1 PPKAVHHPISDHEATLRCWALGFYPAEITLTWQDGEQOTDELVETRPAGDGTQK 60

QY 244 WAAVVPVSGEEQRYTCHVQHEGLPQPL 270
DB 61 WAAVVPVSGEEQRYTCHVQHEGLPQPL 87

RESULT 11
Q29958 PRELIMINARY; PRT; 316 AA.
AC Q29958;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE HLA-C protein (Fragment).
GN HLA-C.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89122144; PubMed=2914713;
```

RA Cianetti L., Testa U., Scotto L., La Valle R., Simeone A., Boccoli G.,  
 RA Giannella G., Feschle C., Borcinelli E.,  
 RT "Three new class I HLA alleles: structure of mRNAs and alternative  
 RT mechanisms of processing.";  
 RL Immunogenetics 29:80-91(1989).  
 CC -1- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE  
 CC IMMUNE SYSTEM (BY SIMILARITY).  
 CC -1- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-  
 CC MICROGLOBULIN) (BY SIMILARITY).  
 CC EMBL; M24096; AAA59654.1; -.  
 DR PIR; C37028; C37028.  
 DR HSSP; P30685; 1A9B.  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR GO; GO:0006955; P:immune response; IEA.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003597; IG-cl.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR InterPro; IPR001039; MHC\_I.  
 DR Pfam; PF00047; IG; 1.  
 DR Pfam; PF00129; MHC I; 1.  
 DR PRINTS; PR01638; MHCCLASSI.  
 DR PRODOM; PD000050; MHC I; 1.  
 DR SMART; SM00407; IGL1; 1.  
 DR PROSITE; PS00835; IG\_LIKE; 1.  
 DR PROSITE; PS00290; IG\_MHC; 1.  
 KW Glycoprotein; Transmembrane.  
 FT NON\_TER 1  
 SQ SEQUENCE 316 AA; 35380 MW; C03B1EC87F75C9BA CRC64;  
 Query Match 26.6%; Score 73; DB 7; Length 316;  
 Best Local Similarity 100.0%; Pred. No. 6.5e-68;  
 Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 195 SDEATLRCWALGFYPAEITLTWQDGEETQDTLVELTRPAGDGTQKWAAVVPSGEE 254  
 DB 169 SDEATLRCWALGFYPAEITLTWQDGEETQDTLVELTRPAGDGTQKWAAVVPSGEE 228  
 QY 255 QRYTCHVQHEGLP 267  
 DB 229 QRYTCHVQHEGLP 241  
 RESULT 12  
 Q860F6 PRELIMINARY; PRT; 314 AA.  
 AC Q860F6;  
 DT 01-JUN-2003 (TREMBlrel. 24, Created)  
 DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)  
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)  
 DE MHC class I antigen (Fragment).  
 GN YANB-A.  
 OS Macaca nemestrina (Pig-tailed macaque).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Euthera; Primates; Catarrhini; Cercopitheciidae;  
 OC Cercopitheciinae; Macaca.  
 OX NCBI\_TaxID=9545;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Lafont B.A.P., Buckler-White A., Pliska R., Buckler C., Martin M.A.;  
 RT "The classical and non-classical MHC class I genes of pig-tailed  
 RT macaques (Macaca nemestrina).";  
 RL Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; AY204730; AAC84319.1; -.  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR GO; GO:0006955; P:immune response; IEA.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003597; IG-cl.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR InterPro; IPR001039; MHC\_I.  
 DR Pfam; PF00047; IG; 1.  
 DR Pfam; PF00129; MHC\_I; 1.  
 DR PRINTS; PR01638; MHCCLASSI.  
 DR PRODOM; PD000050; MHC I; 1.

DR SMART; SM00407; IGL1; 1.  
 DR PROSITE; PS00835; IG\_LIKE; 1.  
 DR PROSITE; PS00290; IG\_MHC; 1.  
 FT NON\_TER 1  
 FT NON\_TER 314 314  
 SQ SEQUENCE 314 AA; 35463 MW; C58S496BA90BDC85 CRC64;  
 Query Match 22.6%; Score 62; DB 7; Length 314;  
 Best Local Similarity 100.0%; Pred. No. 2.4e-56;  
 Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 191 HHPISDHEATLRCWALGFYPAEITLTWQDGEETQDTLVELTRPAGDGTQKWAAVVVP 250  
 DB 183 HHPISDHEATLRCWALGFYPAEITLTWQDGEETQDTLVELTRPAGDGTQKWAAVVVP 242  
 QY 251 SG 252  
 DB 243 SG 244  
 RESULT 13  
 Q9MXS7 PRELIMINARY; PRT; 353 AA.  
 AC Q9MXS7;  
 DT 01-OCT-2000 (TREMBlrel. 15, Created)  
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)  
 DE MHC class I heavy chain antigen (Fragment).  
 GN MAMU-A.  
 OS Macaca mulatta (Rhesus macaque).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Euthera; Primates; Catarrhini; Cercopitheciidae;  
 OC Cercopitheciinae; Macaca.  
 OX NCBI\_TaxID=9544;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=20260989; PubMed=10803844;  
 RA Urvater J.A., McAdam S.N., Loehke J.H., Allen T.M., Moran J.L.,  
 RA Rowell T.J., Rojo S., Lopez de Castro J.A., Taurag J.D., Watkins D.I.;  
 RT "A high incidence of Shigella-induced arthritis in a primate species:  
 RT major histocompatibility complex class I molecules associated with  
 RT resistance and susceptibility, and their relationship to HLA-B\*27.";  
 RL Immunogenetics 51:314-325(2000).  
 CC -1- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE  
 CC IMMUNE SYSTEM (BY SIMILARITY).  
 CC -1- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-  
 CC MICROGLOBULIN) (BY SIMILARITY).  
 CC EMBL; AF157399; AAF71168.1; -.  
 DR HSSP; P30685; 1A9B.  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR GO; GO:0006955; P:immune response; IEA.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003597; IG-cl.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR InterPro; IPR001039; MHC\_I.  
 DR Pfam; PF00047; IG; 1.  
 DR Pfam; PF00129; MHC I; 1.  
 DR PRINTS; PR01638; MHCCLASSI.  
 DR PRODOM; PD000050; MHC I; 1.  
 DR SMART; SM00407; IGL1; 1.  
 DR PROSITE; PS00835; IG\_LIKE; 1.  
 DR PROSITE; PS00290; IG\_MHC; 1.  
 KW Glycoprotein; Transmembrane.  
 FT NON\_TER 1  
 SQ SEQUENCE 353 AA; 39448 MW; ECL1A0A7DB085F5B7 CRC64;  
 Query Match 22.3%; Score 61; DB 7; Length 353;  
 Best Local Similarity 100.0%; Pred. No. 3e-55;  
 Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 195 SDEATLRCWALGFYPAEITLTWQDGEETQDTLVELTRPAGDGTQKWAAVVPSGEE 254  
 DB 207 SDEATLRCWALGFYPAEITLTWQDGEETQDTLVELTRPAGDGTQKWAAVVPSGEE 266

GN MAMU-A.  
 OS Macaca mulatta (Rhesus macaque).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
 OC Cercopithecinae; Macaca.  
 OX NCBI\_TaxID=9544;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20260989; PubMed=10803844;  
 RA Urvater J.A., McAdam S.N., Loehrke J.H., Allen T.M., Moran J.L.,  
 RA Rowell T.J., Rojo S., Lopez de Castro J.A., Taurag J.D., Watkins D.I.;  
 RT "A high incidence of Shigella-induced arthritis in a primate species;  
 RT major histocompatibility complex class I molecules associated with  
 RT resistance and susceptibility, and their relationship to HLA-B\*27.";  
 RL Immunogenetics 51:314-325(2000).  
 CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE  
 CC IMMUNE SYSTEM (BY SIMILARITY).  
 CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-  
 CC MICROGLOBULIN) (BY SIMILARITY).  
 DR EMBL; AF157401; AAF71170.1; -.  
 DR HSP; P30685; IAGS.  
 DR GO; GO:0016021; C: integral to membrane; IEA.  
 DR GO; GO:0006955; P: immune response; IEA.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003597; Ig cl.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR001039; MHC\_I.  
 DR Pfam; PF00047; Ig; 1.  
 DR Pfam; PF00129; MHC\_I; 1.  
 DR PRINTS; PR01638; MHCCLASSI.  
 DR PRODOM; PD000050; MHC\_I; 1.  
 DR SMART; SM00407; IGL1; 1.  
 DR PROSITE; PS00835; IG\_LIKE; 1.  
 DR PROSITE; PS00290; IG\_MHC; 1.  
 DR Glycoprotein; Transmembrane.  
 KW Glycoprotein; Transmembrane.  
 SQ SEQUENCE 365 AA; 40772 MW; 5B7D7D45B8BC284C CRC64;  
 Query Match 22.3%; Score 61; DB 7; Length 365;  
 Best Local Similarity 100.0%; Pred. No. 3le-55;  
 Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 195 SDHEATLRGKALGFYPAEITLTWQDGEQTDTELVEPRAGDGTGKAAVVPVSGEE 254  
 Db 219 SDHEATLRGKALGFYPAEITLTWQDGEQTDTELVEPRAGDGTGKAAVVPVSGEE 278  
 QY 255 Q 255  
 Db 279 Q 279  
 Search completed: June 18, 2004, 19:31:21  
 Job time : 46 secs

QY 255 Q 255  
 Db 267 Q 267  
 RESULT 14  
 Q9MXS6 PRELIMINARY; PRT; 353 AA.  
 AC Q9MXS6;  
 DT 01-OCT-2000 (TREMBlrel. 15, Created)  
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)  
 DE MHC class I heavy chain antigen (fragment).  
 GN MAMU-A.  
 OS Macaca mulatta (Rhesus macaque).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
 OC Cercopithecinae; Macaca.  
 OX NCBI\_TaxID=9544;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20260989; PubMed=10803844;  
 RA Urvater J.A., McAdam S.N., Loehrke J.H., Allen T.M., Moran J.L.,  
 RA Rowell T.J., Rojo S., Lopez de Castro J.A., Taurag J.D., Watkins D.I.;  
 RT "A high incidence of Shigella-induced arthritis in a primate species;  
 RT major histocompatibility complex class I molecules associated with  
 RT resistance and susceptibility, and their relationship to HLA-B\*27.";  
 RL Immunogenetics 51:314-325(2000).  
 CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE  
 CC IMMUNE SYSTEM (BY SIMILARITY).  
 CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-  
 CC MICROGLOBULIN) (BY SIMILARITY).  
 DR EMBL; AF157400; AAF71169.1; -.  
 DR HSP; P30685; IAGS.  
 DR GO; GO:0016021; C: integral to membrane; IEA.  
 DR GO; GO:0006955; P: immune response; IEA.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003597; Ig cl.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR001039; MHC\_I.  
 DR Pfam; PF00047; Ig; 1.  
 DR Pfam; PF00129; MHC\_I; 1.  
 DR PRINTS; PR01638; MHCCLASSI.  
 DR PRODOM; PD000050; MHC\_I; 1.  
 DR SMART; SM00407; IGL1; 1.  
 DR PROSITE; PS00835; IG\_LIKE; 1.  
 DR PROSITE; PS00290; IG\_MHC; 1.  
 DR Glycoprotein; Transmembrane.  
 KW Glycoprotein; Transmembrane.  
 FT NON\_TER 1  
 SQ SEQUENCE 353 AA; 39387 MW; 4F1A6D397F71FEA3 CRC64;  
 Query Match 22.3%; Score 61; DB 7; Length 353;  
 Best Local Similarity 100.0%; Pred. No. 3e-55;  
 Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 195 SDHEATLRGKALGFYPAEITLTWQDGEQTDTELVEPRAGDGTGKAAVVPVSGEE 254  
 Db 207 SDHEATLRGKALGFYPAEITLTWQDGEQTDTELVEPRAGDGTGKAAVVPVSGEE 266  
 QY 255 Q 255  
 Db 267 Q 267  
 RESULT 15  
 Q9MXS5 PRELIMINARY; PRT; 365 AA.  
 AC Q9MXS5;  
 DT 01-OCT-2000 (TREMBlrel. 15, Created)  
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)  
 DE MHC class I heavy chain antigen.

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 18, 2004, 19:26:37 ; Search time 17 Seconds  
(without alignments)

839.248 Million cell updates/sec

Title: US-09-819-371-5

Perfect score: 274

Sequence: 1 GSHSLRYSTAVSRPGRGP.....QRYTCHVQHEGLPOLILRW 274

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 141681 seqs, 52070155 residues

Word size : 0

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : SwissProt\_42.4

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	274	100.0	362	1	HLAF_HUMAN
2	136	46.0	346	1	LC28_PANTR
3	59	21.5	348	1	HLAF_MACMU
4	44	16.1	362	1	HLAF_HUMAN
5	44	16.1	365	1	LA01_HUMAN
6	44	16.1	365	1	LA01_PANTR
7	44	16.1	365	1	LA03_HUMAN
8	44	16.1	365	1	LA03_PANTR
9	44	16.1	365	1	LA04_PANTR
10	44	16.1	365	1	LA11_HUMAN
11	44	16.1	365	1	LA23_HUMAN
12	44	16.1	365	1	LA24_HUMAN
13	44	16.1	365	1	LA30_HUMAN
14	44	16.1	365	1	LA36_HUMAN
15	44	16.1	366	1	LC02_HUMAN
16	44	16.1	366	1	LC03_HUMAN
17	44	16.1	366	1	LC04_HUMAN
18	44	16.1	366	1	LC05_HUMAN
19	44	16.1	366	1	LC06_HUMAN
20	44	16.1	366	1	LC08_HUMAN
21	44	16.1	366	1	LC12_HUMAN
22	44	16.1	366	1	LC14_HUMAN
23	44	16.1	366	1	LC15_HUMAN
24	44	16.1	366	1	LC16_HUMAN
25	44	16.1	366	1	LC18_HUMAN
26	43	15.7	358	1	HLAE_PONPY
27	40	14.6	359	1	HLAE_HUMAN
28	39	14.2	338	1	HLAG_HUMAN
29	37	13.5	365	1	LC01_GORGO
30	32	11.7	359	1	LB01_PANTR
31	32	11.7	362	1	LA02_PANTR
32	32	11.7	362	1	LB01_GORGO
33	32	11.7	362	1	LB02_GORGO

#### ALIGNMENTS

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RESULT 1
HLAF_HUMAN          34      32      11.7      362      1      LB02_PANTR      P13751 pan troglod
AC P30511;          35      32      11.7      362      1      LB03_GORGO      P30381 gorilla gor
DT 01-APR-1993 (Rel. 25, Created)          36      32      11.7      362      1      LB07_HUMAN      P01889 homo sapien
DT 28-FEB-2003 (Rel. 41, Last annotation update)          37      32      11.7      362      1      LB08_HUMAN      P30460 homo sapien
DE HLA class I histocompatibility antigen, alpha chain F precursor (HLA F          38      32      11.7      362      1      LB13_HUMAN      P30461 homo sapien
DE antigen) (leukocyte antigen F) (CDA12).          39      32      11.7      362      1      LB14_HUMAN      P30462 homo sapien
GN HLA-F OR HLAF OR HLA-F.5.4.          40      32      11.7      362      1      LB15_HUMAN      P30464 homo sapien
OS Homo sapiens (Human).          41      32      11.7      362      1      LB18_HUMAN      P30466 homo sapien
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;          42      32      11.7      362      1      LB27_HUMAN      P03989 homo sapien
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.          43      32      11.7      362      1      LB37_HUMAN      P18463 homo sapien
OX NCBI_TaxID=9606;          44      32      11.7      362      1      LB38_HUMAN      Q95365 homo sapien
RN [1]          45      32      11.7      362      1      LB39_HUMAN      P30475 homo sapien
RP SEQUENCE FROM N.A. MEDLINE=90111605; PubMed=1688605;
RX Geraghty D.E., Wei X., Orr H.T., Koller B.H.;
RA "Human leukocyte antigen F (HLA-F). An expressed HLA gene composed of
RT a class I coding sequence linked to a novel transcribed repetitive
RT element."
RL J. Exp. Med. 171:1-18(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=91197889; PubMed=1707659;
RA Lury D., Epstein H., Holmes N.;
RT "The human class I MHC gene HLA-F is expressed in lymphocytes.";
RL Int. Immunol. 2:531-537(1990).
RN [3]
RP SEQUENCE FROM N.A.
RA Shiina S., Tamiya G., Oka A., Inoko H.;
RT "Homo sapiens 2,229,817bp genomic DNA of 6p21.3 HLA class I region.";
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Involved in the presentation of foreign antigens to the
CC immune system.
CC -!- SUBUNIT: Heterodimer of an alpha chain and a beta chain (beta-2-
CC microglobulin).
CC
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CC
CC EMBL; X17093; CAA34947.1; -.
CC EMBL; AF000521; BAB63337.1; -.
CC FIR; A60384; A60384.
CC HSSP; Q30201; IAE2.
CC Genew; HGNC:4963; HLA-F.
CC MIM; 143110; -.
CC GO; GO:0030106; F:MHC class I receptor activity; TAS.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003597; Ig cl.
CC InterPro; IPR003006; Ig_MHC.

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DR InterPro: IPR001039; MHC_I.
DR Pfam: PF00047; Ig; 1.
DR Pfam: PF00129; MHC_I; 1.
DR PRINTS: PR01638; MHCCLASSI.
DR PRODOR: PD000050; MHC_I; 1.
DR SMART: SM00407; IGC1; 1.
DR PROSITE: PS00835; IG_LIKE; 1.
DR PROSITE: PS00290; IG_MHC; 1.
KW MHC I; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 21
FT CHAIN 22 362
FT
FT HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
FT ALPHA CHAIN F.
FT DOMAIN 22 111
FT EXTRACELLULAR ALPHA-1.
FT DOMAIN 112 203
FT EXTRACELLULAR ALPHA-2.
FT DOMAIN 204 295
FT EXTRACELLULAR ALPHA-3.
FT DOMAIN 296 305
FT CONNECTING PEPTIDE.
FT TRANSMEM 306 329
FT CYTOPLASMIC TAIL.
FT DOMAIN 330 362
FT BY SIMILARITY.
FT DISULFID 122 185
FT DISULFID 224 280
FT BY SIMILARITY.
FT CARBOHYD 107 107
FT N-LINKED (GLCNAC...) (BY SIMILARITY).
SQ SEQUENCE 362 AA; 40568 MW; B8DD041F820A34E1 CRC64;

Query Match 100.0%; Score 274; DB 1; Length 362;
Best Local Similarity 100.0%; Pred. No. 1.8e-279;
Matches 274; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GSHSLRYFSTAVSRPGEGEPYIAVEYVDDTQFLRFDSDAAIPRMEPRPWPQEGPQYW 60
Db 22 GSHSLRYFSTAVSRPGEGEPYIAVEYVDDTQFLRFDSDAAIPRMEPRPWPQEGPQYW 81

Qy 61 EWTGYAKANAQTDRLVALNLLRRYNOSEAGSHTLQNGCGDMPDGLRLRGYHQAIDG 120
Db 82 EWTGYAKANAQTDRLVALNLLRRYNOSEAGSHTLQNGCGDMPDGLRLRGYHQAIDG 141

Qy 121 KDYISLNEDLSRWTAADTVQAQITQRFYEAEBEYAEFFTYLEGECELELLRRYLENGKETLQ 180
Db 142 KDYISLNEDLSRWTAADTVQAQITQRFYEAEBEYAEFFTYLEGECELELLRRYLENGKETLQ 201

Qy 181 RADPPKARVHPHPSDHEATLRCWALGFYPAEITLTWQDGEETQDTLVEPRPADGDT 240
Db 202 RADPPKARVHPHPSDHEATLRCWALGFYPAEITLTWQDGEETQDTLVEPRPADGDT 261

Qy 241 FOKWAAVVPVSGEQRVYCHVQHEGLPQLLRW 274
Db 262 FOKWAAVVPVSGEQRVYCHVQHEGLPQLLRW 295

RESULT 2
1C28 PANTR
ID 1C28 PANTR STANDARD; PRT; 346 AA.
AC P16215;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-APR-1993 (Rel. 25, Last annotation update)
DE CHLA class I histocompatibility antigen, CH28 alpha chain precursor.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90201944; PubMed=1690682;
RA Lawlor D.A., Warren E., Ward F.E., Parham P.;
RT "Comparison of class I MHC alleles in humans and apes.";
RL Immunol. Rev. 113:147-185(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=88319000; PubMed=3412487;
RA Lawlor D.A., Ward F.E., Ennis P.D., Jackson A.P., Parham P.;
RT "HLA-A and B polymorphisms predate the divergence of humans and
RT chimpanzees.";
RL Nature 335:268-271(1988).

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CC -!- FUNCTION: Involved in the presentation of foreign antigens to the
CC immune system.
CC -!- SUBUNIT: Heterodimer of an alpha chain and a beta chain (beta-2-
CC microglobulin).
CC
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CC
CC EMBL; Q30685; AAA87973.1; -
CC HSSP; Q30201; 1A6Z.
CC InterPro: IPR007110; IG-like.
CC InterPro: IPR003597; IG_c1.
CC InterPro: IPR003006; IG_MHC.
CC InterPro: IPR001039; MHC_I.
CC Pfam; PF00047; Ig; 1.
CC PRINTS; PR01638; MHCCLASSI.
CC PRODOR; PD000050; MHC_I; 1.
CC SMART; SM00407; IGC1; 1.
CC PROSITE; PS00835; IG_LIKE; 1.
CC PROSITE; PS00290; IG_MHC; 1.
KW MHC I; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 21
FT CHAIN 22 346
FT
FT CHLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
FT CH28 ALPHA CHAIN.
FT DOMAIN 22 111
FT EXTRACELLULAR ALPHA-1.
FT DOMAIN 112 203
FT EXTRACELLULAR ALPHA-2.
FT DOMAIN 204 295
FT EXTRACELLULAR ALPHA-3.
FT DOMAIN 296 305
FT CONNECTING PEPTIDE.
FT TRANSMEM 306 329
FT CYTOPLASMIC TAIL.
FT DOMAIN 330 346
FT BY SIMILARITY.
FT DISULFID 122 185
FT DISULFID 224 280
FT BY SIMILARITY.
FT CARBOHYD 107 107
FT N-LINKED (GLCNAC...) (BY SIMILARITY).
SQ SEQUENCE 346 AA; 39084 MW; F83E882D5C2E0971 CRC64;

Query Match 46.0%; Score 126; DB 1; Length 346;
Best Local Similarity 100.0%; Pred. No. 3.4e-124;
Matches 126; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 63 TTGYAKANAQTDRLVALNLLRRYNOSEAGSHTLQNGCGDMPDGLRLRGYHQAIDGKD 122
Db 84 TTGYAKANAQTDRLVALNLLRRYNOSEAGSHTLQNGCGDMPDGLRLRGYHQAIDGKD 143

Qy 123 YISLNEDLSRWTAADTVQAQITQRFYEAEBEYAEFFTYLEGECELELLRRYLENGKETLQRA 182
Db 144 YISLNEDLSRWTAADTVQAQITQRFYEAEBEYAEFFTYLEGECELELLRRYLENGKETLQRA 203

Qy 183 DPPKAH 188
Db 204 DPPKAH 209

RESULT 3
HLAF_MACMU
ID HLAF_MACMU STANDARD; PRT; 348 AA.
AC P33617;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE HLA class I histocompatibility antigen, alpha chain F precursor (HLA F
DE antigen) (leukocyte antigen F).
GN HLA-F OR HLAF.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheidae; Macaca.
OX NCBI_TaxID=9544;

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RN  SEQUENCE FROM N.A.
RP  MEDLINE=93246295; PubMed=8482576;
RX  Otting N., Bontrop R.E.;
RA  "Characterization of the rhesus macaque (Macaca mulatta) equivalent
RT  of HLA-F.";
RL  Immunogenetics 38:141-145(1993).
CC  -!- FUNCTION: Involved in the presentation of foreign antigens to the
CC  immune system.
CC  -!- SUBUNIT: Heterodimer of an alpha chain and a beta chain (beta-2-
CC  microglobulin).
CC  -----
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CC  entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC  or send an email to license@isb-sib.ch).
CC  -----
DR  EMBL; Z21819; CAA79885.1; -
DR  PIR; S29990; S29990.
DR  HSSP; Q30201; IAGZ.
DR  InterPro; IPR007110; IG-like.
DR  InterPro; IPR003597; IG-cl.
DR  InterPro; IPR003006; IG_MHC.
DR  InterPro; IPR001039; MHC_I.
DR  Pfam; PF00047; ig; 1.
DR  Pfam; PF00129; MHC_I.1.
DR  PRINTS; PR01638; MHCCLASSI.
DR  ProDom; PD000050; MHC_I.1.
DR  SMART; SM00407; IGC1; 1.
DR  PROSITE; PS08335; IG LIKE; 1.
DR  PROSITE; PS00290; IG_MHC; 1.
KW  MHC I; Transmembrane; Glycoprotein; Signal.
FT  SIGNAL 1 21
FT  CHAIN 22 348
FT  HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
FT  ALPHA CHAIN F.
FT  DOMAIN 22 113
FT  DOMAIN 114 205
FT  DOMAIN 206 297
FT  DOMAIN 298 307
FT  DOMAIN 308 331
FT  TRANSMEM 332 348
FT  DISULFID 124 187
FT  DISULFID 226 282
FT  CARBOHYD 109 109
FT  SEQUENCE 348 AA; 39300 MW; 77BD7E3B9B11E0F7 CRC64;
Query Match 21.5%; Score 59; DB 1; Length 348;
Best Local Similarity 100.0%; Pred. No. 6.8e-54;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 212 EITLTWRDGEETQDTVELVETPAGDGTGFKWAAVVPVSGEQRVYCHVQHEGLPQL 270
DB 235 EITLTWRDGEETQDTVELVETPAGDGTGFKWAAVVPVSGEQRVYCHVQHEGLPQL 293
RESULT 4
HLAH HUMAN STANDARD; PRT; 362 AA.
AC P01893;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE HLA class I histocompatibility antigen, alpha chain H precursor
DE (HLA-AR) (HLA-12.4).
GN HLA-H OR HLAH.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
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RP  SEQUENCE FROM N.A.
RX  MEDLINE=92151002; PubMed=6461010;
RA  Malissen M., Malissen B., Jordan B.R.;
RT  "Exon/intron organization and complete nucleotide sequence of an HLA
RT  gene.";
RL  Proc. Natl. Acad. Sci. U.S.A. 79:893-897(1982).
CC  -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC  THE IMMUNE SYSTEM. COULD BE THE PRODUCT OF A PSEUDOGENE.
CC  -!- SUBUNIT: Heterodimer of an alpha chain and a beta chain (beta-2-
CC  microglobulin).
CC  -----
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CC  -----
DR  EMBL; J00191; AAA36218.1; ALT_INIT.
DR  HSSP; P03989; IHSA.
DR  Genew; HGNC:4965; HLA-H.
DR  XIM; 142800.
DR  GO; GO:0005887; C: integral to plasma membrane; NAS.
DR  GO; GO:0030106; F: MHC class I receptor activity; NAS.
DR  GO; GO:0006955; P: immune response; NAS.
DR  InterPro; IPR007110; IG-like.
DR  InterPro; IPR003597; IG-cl.
DR  InterPro; IPR003006; IG_MHC.
DR  InterPro; IPR001039; MHC_I.
DR  Pfam; PF00047; ig; 1.
DR  Pfam; PF00129; MHC_I.1.
DR  PRINTS; PR01638; MHCCLASSI.
DR  ProDom; PD000050; MHC_I.1.
DR  SMART; SM00407; IGC1; 1.
DR  PROSITE; PS08335; IG LIKE; 1.
DR  PROSITE; PS00290; IG_MHC; 1.
KW  MHC I; Transmembrane; Glycoprotein; Signal.
FT  SIGNAL 1 24
FT  CHAIN 25 362
FT  HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
FT  ALPHA CHAIN H.
FT  DOMAIN 25 114
FT  DOMAIN 115 206
FT  DOMAIN 207 298
FT  DOMAIN 299 308
FT  TRANSMEM 309 332
FT  DOMAIN 333 362
FT  CARBOHYD 110 110
FT  DISULFID 227 283
FT  SEQUENCE 362 AA; 40850 MW; 0BCDAE8D61A81B86 CRC64;
Query Match 16.1%; Score 44; DB 1; Length 362;
Best Local Similarity 100.0%; Pred. No. 3.9e-38;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 224 QTQDTVELVETPAGDGTGFKWAAVVPVSGEQRVYCHVQHEGLP 267
DB 248 QTQDTVELVETPAGDGTGFKWAAVVPVSGEQRVYCHVQHEGLP 291
RESULT 5
LA01 HUMAN STANDARD; PRT; 365 AA.
ID LA01 HUMAN
AC P30433; O77964; O78171; Q9MYA3; Q9TP25; Q9TP5;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE HLA class I histocompatibility antigen, A-1 alpha chain precursor
DE (MHC class I antigen A*1).
GN HLA-A OR HLAH.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
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OX NCBI\_TaxID=9606;  
RN [1] SEQUENCE FROM N.A. (A\*0101).  
RP MEDLINE=88234547; PubMed=3375250;  
RX Parham P., Lomen C.E., Lawlor D.A., Ways J.P., Holmes N., Coppin H.L.,  
RA Salter R.D., Wan A.M., Ennis P.D.;  
RT "Nature of polymorphism in HLA-A, -B, and -C molecules.";  
RL Proc. Natl. Acad. Sci. U.S.A. 85:4005-4009(1988).  
RN [2] SEQUENCE FROM N.A. (A\*0101).  
RP MEDLINE=8923215; PubMed=2715640;  
RX Parham P., Lawlor D.A., Lomen C.E., Ennis P.D.;  
RA "Diversity and diversification of HLA-A,B,C alleles.";  
RT J. Immunol. 142:3937-3950(1989).  
RN [3] SEQUENCE FROM N.A. (A\*0101).  
RP Warren E.;  
RA Submitted (APR-1989) to the EMBL/GenBank/DBJ databases.  
RN [4] SEQUENCE FROM N.A. (A\*0101).  
RP MEDLINE=91067475; PubMed=2251137;  
RX Girdestone J.;  
RA "Nucleotide sequence of an HLA-A1 gene.";  
RL Nucleic Acids Res. 18:6701-6701(1990).  
RN [5] SEQUENCE FROM N.A. (A\*0101).  
RP MEDLINE=98007773; PubMed=9349617;  
RX Laforet M., Froelich N., Parisiadis A., Pfeiffer B., Schell A.,  
RA Falier B., Woehl-Jaegle M.L., Cazenave J.P., Tongio M.M.;  
RT "A nucleotide insertion in exon 4 is responsible for the absence of  
expression of an HLA-A\*01 allele.";  
RL Tissue Antigens 50:347-350(1997).  
RN [6] SEQUENCE FROM N.A. (A\*0101).  
RP Waller M.J., Robinson J., Marsh S.G.E.;  
RA Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.  
RN [7] SEQUENCE FROM N.A. (A\*0101).  
RP TISSUE=Brain;  
RX MEDLINE=22386257; PubMed=12477932;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan T.B., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diachenko L., Marushina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Schetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahy J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,  
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length  
human and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [8] SEQUENCE FROM N.A. (A\*0102).  
RP MEDLINE=95282145; PubMed=7761977;  
RX Browning M.J., Madrigal J.A., Krausa P., Kowalski H.,  
RA Allsopp C.E., Little A.-M., Turner S., Adams E.J., Arnett K.L.,  
RA Bodmer W.F., Parham P.;  
RT "The HLA-A,B,C genotype of the class I negative cell line Daudi  
reveals novel HLA-A and -B alleles.";  
RL Tissue Antigens 45:177-187(1995).  
RN [9] SEQUENCE OF 26-206 FROM N.A. (A\*0103).  
RX MEDLINE=98101100; PubMed=9438203;  
RA Sitha S., Scheltinga S.A., Johnston-Dow L.A., White C.B.,  
der van Zwan A.W., Bakema J.E., Rozemuller E.H., van der Tweel J.G.,  
RA Kronink M.N., Tilanus M.G.J.;  
RT "A generic sequencing based typing approach for the identification of  
HLA-A diversity.";  
RL Hum. Immunol. 57:120-128(1997).  
RN [10] SEQUENCE OF 26-206 FROM N.A. (A\*0103).  
RP TISSUE=Blood;  
RX MEDLINE=21100775; PubMed=11182232;  
RA Poland G.A., Sohni Y., Domanic M., Kroning C.M., DeGoey S.R.,  
RA Jimale M., Jacobson R.M., Moore S.B.;  
RT "High frequency of HLA-A\*0103 allele in a Somali population.";  
RL Hum. Immunol. 62:197-200(2001).  
RN [11] SEQUENCE OF 26-206 FROM N.A. (A\*0106).  
RP MEDLINE=20309230; PubMed=10852390;  
RX Ellis J., Steiner N.K., Kosman C., Henson V., Mitton W., Koester R.,  
RA NG J., Hartzman R.J., Hurley C.K.;  
RT "Seventeen more novel HLA-A locus alleles.";  
RL Tissue Antigens 55:369-373(2000).  
RN [12] SEQUENCE OF 26-206 FROM N.A. (A\*0107).  
RP Tamouza R., Fortier C., Mahfoudh N., Schaeffer V., Poirier J.C.,  
RA Marais F., Gautreau C., Charron D.;  
RT "A new HLA-A\*01 allele.";  
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.  
RN [13] SEQUENCE OF 26-206 FROM N.A. (A\*0107).  
RP MEDLINE=88088800; PubMed=3121736;  
RX Sant A.J., Zacheis M., Rumbarger T., Giacoletto K.S., Schwartz B.D.;  
RT "Human Ia alpha- and beta-chains are sulfated.";  
RL J. Immunol. 140:155-160(1988).  
CC -!- FUNCTION: Involved in the presentation of foreign antigens to  
the immune system.  
CC -!- SUBUNIT: Dimer of alpha chain and a beta chain (beta-2-  
microglobulin).  
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -!- PTM: Sulfated.  
CC -!- POLYMORPHISM: The following alleles of A-1 are known: A\*0101,  
A\*0102, A\*0103, A\*0106 and A\*0107. The sequence shown is that of  
A\*0101.  
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EMBL; M24043; AAA59652.1; -  
EMBL; X55710; CAA39243.1; -  
EMBL; Z93949; CAB07989.1; -  
EMBL; AJ278305; CAB93537.1; -  
EMBL; BC003069; AAH03069.1; -  
EMBL; U07161; AAA80569.1; -  
EMBL; Y12469; CAA73072.1; -  
EMBL; Y12470; CAA73073.1; -  
EMBL; AF214112; AAF19525.1; -  
EMBL; AF214111; AAF19525.1; JOINED.  
EMBL; AF143232; AAD33894.1; -  
EMBL; AF143231; AAD33894.1; JOINED.  
EMBL; AF219633; AAF73862.1; -  
EMBL; AF219632; AAF73862.1; JOINED.  
PIR; I38518; I38518.  
PIR; I61856; I61856.  
HSP; O19673; IHSB.  
Gene; HGNC:4931; HLA-A.  
MIN; 142800; -  
GO; GO:0005887; C:integral to plasma membrane; NAS.  
GO; GO:0030106; F:MHC class I receptor activity; NAS.  
GO; GO:0006955; P:immune response; NAS.  
InterPro; IPR007110; Ig-like.

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DR InterPro; IPR003597; IG cl.
DR InterPro; IPR003006; IG MHC.
DR Pfam; PF00047; ig; 1.
DR Pfam; PF00129; MHC_I; 1.
DR PRINTS; PR01638; MHCCLASSI.
DR PRODOM; PD000050; MHC_I; 1.
DR SMART; SM00407; IGI1; 1.
DR PROSITE; PS00835; IG LIKE; 1.
DR PROSITE; PS00290; IG MHC; 1.
KW MHC I; Transmembrane; Glycoprotein; Signal; Polymorphism.
FT SIGNAL 1 24
FT CHAIN 25 365
FT HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
FT A-1 ALPHA CHAIN.
FT DOMAIN 25 114
FT EXTRACELLULAR ALPHA-1.
FT DOMAIN 115 206
FT EXTRACELLULAR ALPHA-2.
FT DOMAIN 207 298
FT EXTRACELLULAR ALPHA-3.
FT DOMAIN 299 308
FT CONNECTING PEPTIDE.
FT TRANSMEM 309 332
FT DOMAIN 333 365
FT CYTOPLASMIC TAIL.
FT MOD RES 83 83
FT CARBOHYD 110 110
FT DISULFID 125 188
FT DISULFID 227 283
FT VARIANT 33 33
FT F -> S (in allele A*0102).
FT /FTid=VAR_004332.
FT R -> S (in allele A*0102).
FT /FTid=VAR_004333.
FT G -> R (in allele A*0107).
FT /FTid=VAR_016719.
FT M -> V (in allele A*0107).
FT /FTid=VAR_016720.
FT A -> E (in allele A*0107).
FT /FTid=VAR_016721.
FT D -> A (in allele A*0107).
FT /FTid=VAR_016722.
FT I -> M (in allele A*0103).
FT /FTid=VAR_016723.
FT R -> L (in allele A*0106).
FT /FTid=VAR_016724.
FT V -> A (in allele A*0106).
FT /FTid=VAR_016725.
SQ SEQUENCE 365 AA; 40846 MW; 8667AFF3F06C4932 CRC64;

Query Match 16.1%; Score 44; DB 1; Length 365;
Best Local Similarity 100.0%; Pred. No. 3.9e-38;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 224 QTQDTLVELTRPAGDGTGFKWAAVVVPSGEEQRYTCHVQHEGLP 267
Dd 248 QTQDTLVELTRPAGDGTGFKWAAVVVPSGEEQRYTCHVQHEGLP 291

RESULT 6
ID LA01 PANTR STANDARD; PRT; 365 AA.
AC P16209;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DE "HLA class I histocompatibility antigen, A-2 alpha chain precursor.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90201944; PubMed=1690682;
RA Lawlor D.A., Warren E., Ward F.E., Parham P.;
RT "Comparison of class I MHC alleles in humans and apes.";
RL Immunol. Rev. 113:147-185(1990).
CC -!- FUNCTION: Involved in the presentation of foreign antigens to the
immune system.

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CC -!- SUBUNIT: Heterodimer of an alpha chain and a beta chain (beta-2-
microglobulin).
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; M30678; AAA87970.1; --
CC PIR; I36961; I36961.
CC HSP; Q95352; IHHK.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003597; IG cl.
CC InterPro; IPR003006; IG MHC.
CC InterPro; IPR001039; MHC_I.
CC Pfam; PF00047; ig; 1.
CC Pfam; PF00129; MHC_I; 1.
CC PRINTS; PR01638; MHCCLASSI.
CC PRODOM; PD000050; MHC_I; 1.
CC SMART; SM00407; IGI1; 1.
CC PROSITE; PS00835; IG LIKE; 1.
CC PROSITE; PS00290; IG MHC; 1.
KW MHC I; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 24
FT CHAIN 25 365
FT HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
FT A-2 ALPHA CHAIN.
FT DOMAIN 25 114
FT EXTRACELLULAR ALPHA-1.
FT DOMAIN 115 206
FT EXTRACELLULAR ALPHA-2.
FT DOMAIN 207 298
FT EXTRACELLULAR ALPHA-3.
FT DOMAIN 299 308
FT CONNECTING PEPTIDE.
FT TRANSMEM 309 332
FT DOMAIN 333 365
FT CYTOPLASMIC TAIL.
FT DISULFID 125 188
FT DISULFID 227 283
FT CARBOHYD 110 110
FT SEQUENCE 365 AA; 40848 MW; FC452786BD038D3E CRC64;

Query Match 16.1%; Score 44; DB 1; Length 365;
Best Local Similarity 100.0%; Pred. No. 3.9e-38;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 224 QTQDTLVELTRPAGDGTGFKWAAVVVPSGEEQRYTCHVQHEGLP 267
Dd 248 QTQDTLVELTRPAGDGTGFKWAAVVVPSGEEQRYTCHVQHEGLP 291

RESULT 7
ID LA03 HUMAN STANDARD; PRT; 365 AA.
AC P04439; O19546; O9GJ66; O9GJ67; O9GJ68; Q9MYG4; Q9TPR8;
DT 13-AUG-1987 (Rel. 05, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE "HLA class I histocompatibility antigen, A-3 alpha chain precursor
DE (MHC class I antigen A*3).
GN HLA-A OR HLA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (A*0301).
RX MEDLINE=84207948; PubMed=6609814;
RA Strachan T., Sodoyer R., Damotte M., Jordan B.R.;
RT "Complete nucleotide sequence of a functional class I HLA gene,
RT HLA-A3; implications for the evolution of HLA genes.";
RL EMBO J. 3:887-894(1984).
RN [2]
RP SEQUENCE FROM N.A. (A*0301).
RA Ellenson M.E., Hildebrand W.H.;

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DR EMBL; X13113; CAA31505.1; ALT_INIT.
DR PIR; S03535; S03535.
DR HSSP; O19673; IHSB.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR001039; MHC_I.
DR Pfam; PF00047; Ig; 1.
DR Pfam; PF00129; MHC_I; 1.
DR PRINTS; PR01638; MHCCLASSI.
DR ProDom; PD000050; MHC_I; 1.
DR SMART; SM00407; IGC1; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
DR PROSITE; PS00290; IG_MHC; 1.
KW MHC I; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 24
FT CHAIN 25 365
FT CHLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
FT A-108 ALPHA CHAIN.
FT DOMAIN 25 114
FT DOMAIN 115 206
FT DOMAIN 207 298
FT DOMAIN 299 308
FT TRANSMEM 309 332
FT DOMAIN 333 365
FT DISULFID 125 188
FT DISULFID 227 283
FT CARBOHYD 110 110
SQ SEQUENCE 365 AA; 40822 MW; 48CC757055221FC3 CRC64;

Query Match 16.1%; Score 44; DB 1; Length 365;
Best Local Similarity 100.0%; Pred. No. 3.9e-38;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 224 QTQDTLVEVTRPAGDGTFOKAAVVVPSGEEQRYTCHVQHEGLP 267
DB 248 QTQDTLVEVTRPAGDGTFOKAAVVVPSGEEQRYTCHVQHEGLP 291

RESULT 9
1A04 PANTR
ID 1A04 PANTR STANDARD; PRT; 365 AA.
AC P13749;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 01-APR-1993 (Rel. 25, Last annotation update)
DE CHLA class I histocompatibility antigen, A-126 alpha chain precursor.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX NCBI_TaxID=9598;
[1]_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89030641; PubMed=2460344;
RA Mayer W.E., Jonker M., Klein D., Ivanyi P., van Seventer G.,
RA Klein J.;
RT "Nucleotide sequences of chimpanzee MHC class I alleles: evidence for
trans-species mode of evolution.";
RL EMBL J. 7:2765-2774(1988).
CC -!- FUNCTION: Involved in the presentation of foreign antigens to the
immune system.
CC -!- SUBUNIT: Heterodimer of an alpha chain and a beta chain (beta-2-
microglobulin).
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DR EMBL; X13114; CAA31506.1; -.
DR PIR; S01171; S01171.
DR HSSP; O19673; IHSB.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR001039; MHC_I.
DR Pfam; PF00047; Ig; 1.
DR Pfam; PF00129; MHC_I; 1.
DR PRINTS; PR01638; MHCCLASSI.
DR ProDom; PD000050; MHC_I; 1.
DR SMART; SM00407; IGC1; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
DR PROSITE; PS00290; IG_MHC; 1.
KW MHC I; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 24
FT CHAIN 25 365
FT CHLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
FT A-126 ALPHA CHAIN.
FT DOMAIN 25 114
FT DOMAIN 115 206
FT DOMAIN 207 298
FT DOMAIN 299 308
FT TRANSMEM 309 332
FT DOMAIN 333 365
FT DISULFID 125 188
FT DISULFID 227 283
FT CARBOHYD 110 110
SQ SEQUENCE 365 AA; 40656 MW; D3C9A810B22A768F CRC64;

Query Match 16.1%; Score 44; DB 1; Length 365;
Best Local Similarity 100.0%; Pred. No. 3.9e-38;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 224 QTQDTLVEVTRPAGDGTFOKAAVVVPSGEEQRYTCHVQHEGLP 267
DB 248 QTQDTLVEVTRPAGDGTFOKAAVVVPSGEEQRYTCHVQHEGLP 291

RESULT 10
1A11 HUMAN
ID 1A11 HUMAN STANDARD; PRT; 365 AA.
AC P13746; O19605; O19606; Q29747; Q29835; Q9ECN0; Q9MYI5; Q9TQE9;
AC Q9TQP6; Q9TQP7;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE HLA class I histocompatibility antigen, A-11 alpha chain precursor
DE (MHC class I antigen A*11).
GN HLA-A OR HLA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (A*1101 AND A*1102).
RX MEDLINE=89030641; PubMed=2460344;
RA Mayer W.E., Jonker M., Klein D., Ivanyi P., van Seventer G.,
RA Klein J.;
RT "Nucleotide sequences of chimpanzee MHC class I alleles: evidence for
trans-species mode of evolution.";
RL EMBL J. 7:2765-2774(1988).
CC [2]
RP SEQUENCE FROM N.A. (A*1101 AND A*1102).
RX MEDLINE=94287401; PubMed=8016845;
RA Lin L., Tokunaga K., Ishikawa Y., Bannai M., Kashiwase K.,
RA Kuwata S., Akaza T., Tadokoro K., Shibata Y., Juji T.;
RT "Sequence analysis of serological HLA-A11 split antigens, A11.1 and
A11.2.";
RL Tissue Antigens 43:78-82(1994).
CC [3]
RP SEQUENCE OF 26-365 FROM N.A. (A*1101).
RP
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FT VARIANT 345 345 T -> S (in allele A*1105).
FT /FTID=VAR_016736.
SQ SEQUENCE 365 AA; 40937 MW; FE449CE2D4BF6CC5 CRC64;

Query Match 16.1%; Score 44; DB 1; Length 365;
Best Local Similarity 100.0%; Pred. No. 3.9e-38;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 224 QTQDTLTVETRPAGDGTQKWAAVVPSGGEQRYTCHVOHEGLP 267
DB 248 QTQDTLTVETRPAGDGTQKWAAVVPSGGEQRYTCHVOHEGLP 291

RESULT 11
1A23 HUMAN STANDARD; PRT; 365 AA.
AC P30447; Q9TQF1; Q9TQF8; Q9TQF5; Q9TQW6;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE HLA class I histocompatibility antigen, A-23 alpha chain precursor
DE (MHC class I antigen A*23) (A-9).
GN HLA-A OR HLA-A.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (A*2301).
RA Little A.-M., Madrigal J.A., Parham P.;
RT "Molecular definition of an elusive third HLA-A9 molecule: HLA-A9.3.";
RL Immunogenetics 35:41-45(1992).
RN [2]
RP SEQUENCE OF 26-206 FROM N.A. (A*2302 AND A*2303).
RX MEDLINE=20309230; PubMed=10852390;
RA Ellis J., Steiner N.K., Kosman C., Henson V., Mitton W., Koester R.,
RA Ng J., Hartzman R.J., Hurley C.K.;
RT "Seventeen more novel HLA-A locus alleles.";
RL Tissue Antigens 55:369-373(2000).
RN [3]
RP SEQUENCE OF 26-206 FROM N.A. (A*2304 AND A*2305).
RX MEDLINE=21068830; PubMed=11169246;
RA Steiner N.K., Edson S.M., Mitton W., Ng J., Hartzman R.J.,
RA Hurley C.K.;
RT "Seven novel HLA-A alleles carry previously observed polymorphisms.";
RL Tissue Antigens 56:1551-552(2000).
CC -1- FUNCTION: Involved in the presentation of foreign antigens to
CC the immune system.
CC -1- SUBUNIT: Heterodimer of an alpha chain and a beta chain (beta-2-
CC microglobulin).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- POLYMORPHISM: The following alleles of A-23 are known: A*2301, of
CC A*2302, A*2303, A*2304 and A*2305. The sequence shown is that
CC A*2301.
CC
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CC
CC EMBL; M64742; AAA03662.1; -
CC EMBL; AF137080; AAD33736.1; -
CC EMBL; AF137079; AAD33736.1; JOINED.
CC EMBL; AF102572; AAD28171.1; -
CC EMBL; AF102571; AAD28171.1; JOINED.
CC EMBL; AF135549; AAD22272.1; -
CC EMBL; AF135548; AAD22272.1; JOINED.
CC EMBL; AF140860; AAD31878.1; -
CC EMBL; AF140859; AAD31878.1; JOINED.
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DR HSPSP; Q95352; IHHK.
DR Genew; HGNC:4931; HLA-A.
DR MIM; 142800; -
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig MHC.
DR InterPro; IPR001039; MHC_I.
DR Pfam; PF00047; Ig; 1.
DR Pfam; PF00129; MHC_I; 1.
DR PRINTS; PR01638; MHCCLASSI.
DR PRODOM; PD000050; MHC_I; 1.
DR SMART; SM00407; IGG1; 1.
DR PROSITE; PS00835; IG LIKE; 1.
DR PROSITE; PS00290; IG MHC; 1.
KW MHC I; Transmembrane; Glycoprotein; Signal; Polymorphism.
FT SIGNAL 1 24
FT CHAIN 25 365 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
FT DOMAIN 25 114 A-23 ALPHA CHAIN.
FT DOMAIN 115 206 EXTRACELLULAR ALPHA-1.
FT DOMAIN 207 298 EXTRACELLULAR ALPHA-2.
FT DOMAIN 299 308 EXTRACELLULAR ALPHA-3.
FT TRANSMEM 309 332 CONNECTING PEPTIDE.
FT DOMAIN 333 365 CYTOPLASMIC TAIL.
FT CARBOHYD 110 110 N-LINKED (GLCNAC. .) (BY SIMILARITY).
FT DISULFID 125 188 BY SIMILARITY.
FT DISULFID 227 283 BY SIMILARITY.
FT VARIANT 31 31 Y -> C (in allele A*2305).
FT VARIANT 151 151 /FTID=VAR_016606.
FT VARIANT 180 180 /FTID=VAR_016607.
FT VARIANT 180 180 /FTID=VAR_016607.
FT VARIANT 180 180 L -> W (in allele A*2302).
FT VARIANT 180 180 /FTID=VAR_016608.
FT VARIANT 190 191 DG -> EW (in allele A*2304).
FT SEQUENCE 365 AA; 40732 MW; C372DE503BF393D0 CRC64;

Query Match 16.1%; Score 44; DB 1; Length 365;
Best Local Similarity 100.0%; Pred. No. 3.9e-38;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 224 QTQDTLTVETRPAGDGTQKWAAVVPSGGEQRYTCHVOHEGLP 267
DB 248 QTQDTLTVETRPAGDGTQKWAAVVPSGGEQRYTCHVOHEGLP 291

RESULT 12
1A24 HUMAN STANDARD; PRT; 365 AA.
AC P05534; P30448; P30449; Q29908; Q29909; Q29910; Q95355;
DT 01-NOV-1988 (Rel. 09, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE HLA class I histocompatibility antigen, A-24 alpha chain precursor
DE (MHC class I antigen A*24) (A-9).
GN HLA-A OR HLA-A.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (A*2401).
RX MEDLINE=85206128; PubMed=2387115;
RA N'Guyen C., Sodoyer R., Trucy J., Strachan T., Jordan B.R.;
RT "The HLA-AW24 gene: sequence, surroundings and comparison with the
RL HLA-A2 and HLA-A3 genes.";
RN [2]
RP Immunogenetics 21:479-489(1985).
RN [2]
RP REVISIONS.
RA Jordan B.R.;
RL Submitted (XXX-1988) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A. (A*2402 AND A*2403).
```

RX MEDLINE=92104637; PubMed=1729171;  
 RA Little A.-M., Madrigal J.A., Parham P.;  
 RT Molecular definition of an elusive third HLA-A9 molecule: HLA-A9.3.";  
 RL Immunogenetics 35:41-45(1992).  
 RN [4]  
 RP SEQUENCE FROM N.A. (A\*2402).  
 RX MEDLINE=92269955; PubMed=1317015;  
 RA Belich M.P., Madrigal J.A., Hilgeland W.H., Zemmour J.,  
 RA Williams R.C., Luz R., Petzl-Erler M.L., Parham P.;  
 RT "Unusual HLA-B alleles in two tribes of Brazilian Indians";  
 RL Nature 357:326-329(1992).  
 RN [5]  
 RP SEQUENCE FROM N.A. (A\*2402).  
 RX MEDLINE=98007772; PubMed=9349616;  
 RA Laforest M., Froelich N., Parissiadis A., Bausinger H., Pfeiffer B.,  
 RA Tongio M.M.;  
 RT "An intronic mutation responsible for a low level of expression of an  
 RL HLA-A\*24 allele";  
 RN Tissue Antigens 50:340-346(1997).  
 RP [6]  
 RP SEQUENCE FROM N.A. (A\*2408).  
 RX TISSUE=Blood;  
 RA Kashiwase K., Tokunaga K., Ishikawa Y., Qiu L., Furuya M.,  
 RA Sawanaka K., Akaza T., Tadokoro K., Juji T.;  
 RT "A new A9 sequence HLA-A9H from Japanese";  
 RL MHC 3:9-14(1996).  
 RN [7]  
 RP SEQUENCE OF 26-206 FROM N.A. (A\*2410).  
 RX TISSUE=Blood;  
 RA Gao X., Matheson B.;  
 RT "A novel HLA-A\*24 (A\*2410) identified in a Javanese population.";  
 RL Tissue Antigens 48:711-713(1996).  
 RN [8]  
 RP SEQUENCE OF 26-206 FROM N.A. (A\*2406; A\*2413 AND A\*2414).  
 RX TISSUE=Blood;  
 RA Matheson B.;  
 RT "Three newly identified A\*24 alleles: A\*2406, A\*2413 and A\*2414.";  
 RL Tissue Antigens 50:192-196(1997).  
 CC -!- FUNCTION: Involved in the presentation of foreign antigens to  
 CC the immune system.  
 CC -!- SUBUNIT: Heterodimer of an alpha chain and a beta chain (beta-2-  
 CC microglobulin).  
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -!- POLYMORPHISM: The following alleles of A-24 are known: A\*2401,  
 CC A\*2402, A\*2403, A\*2406, A\*2408 (A9H), A\*2410 (A\*240V), A\*2413  
 CC (A\*24YM) and A\*2414 (A\*24SA). Allele A\*2402 is represented in all  
 CC major racial groups. Allele A\*2406 and allele A\*2413 are found in  
 CC the Australian Aboriginal population. Allele A\*2414 is found in  
 CC individuals of South American descent. The sequence shown is that  
 CC of A\*2402.  
 CC -----  
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 CC -----  
 DR EMBL; M15497; AAA59611.1; -;  
 DR EMBL; M64740; AAA59600.1; -;  
 DR EMBL; M64741; AAA59601.1; -;  
 DR EMBL; Z72422; CAA96532.1; -;  
 DR EMBL; D83516; BAA11936.1; -;  
 DR EMBL; U37111; AAA83264.1; -;  
 DR EMBL; U37110; AAA83264.1; JOINED.  
 DR EMBL; U37113; AAA83265.1; -;  
 DR EMBL; U37112; AAA83265.1; JOINED.  
 DR EMBL; U37115; ABA40048.1; -;  
 DR EMBL; U37114; ABA40048.1; JOINED.  
 DR EMBL; U19733; AAB60651.1; -;

DR EMBL; U18987; AAB60651.1; JOINED.  
 DR PIR; I54416; I54416.  
 DR HSSP; Q95352; 1HHK.  
 DR Genew; HGNC:4931; HLA-A.  
 DR MIM; 142800; -;  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003597; IG-cl.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR InterPro; IPR001039; MHC\_I.  
 DR Pfam; PF00047; IG; 1.  
 DR Pfam; PF00129; MHC\_I; 1.  
 DR PRINTS; PR01638; MHCCLASSI.  
 DR ProDom; PD000050; MHC\_I; 1.  
 DR SMART; SM00407; IGcl\_1.  
 DR PROSITE; PS00835; IG\_LIKE; 1.  
 DR PROSITE; PS00290; IG\_MHC; 1.  
 KW MHC I; Transmembrane; Glycoprotein; Signal; Polymorphism.  
 FT SIGNAL 1 24  
 FT CHAIN 25 365 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,  
 FT A-24 ALPHA CHAIN.  
 FT DOMAIN 25 114 EXTRACELLULAR ALPHA-1.  
 FT DOMAIN 115 206 EXTRACELLULAR ALPHA-2.  
 FT DOMAIN 207 298 EXTRACELLULAR ALPHA-3.  
 FT DOMAIN 299 308 CONNECTING PEPTIDE.  
 FT TRANSMEM 309 332  
 FT DOMAIN 333 365 CYTOPLASMIC TAIL.  
 FT CARBOHYD 110 110 N-LINKED (GLCNAC. .) (BY SIMILARITY).  
 FT DISULFID 125 188 BY SIMILARITY.  
 FT DISULFID 227 283 BY SIMILARITY.  
 FT VARIANT 5 5 A -> G (in allele A\*2401).  
 FT VARIANT 27 27 /FTID=VAR\_004354.  
 FT VARIANT 86 86 H -> Q (in allele A\*2408).  
 FT VARIANT 89 89 E -> G (in allele A\*2408).  
 FT VARIANT 89 89 /FTID=VAR\_004356.  
 FT VARIANT 119 119 G -> R (in allele A\*2408).  
 FT VARIANT 121 121 /FTID=VAR\_004357.  
 FT VARIANT 121 121 L -> V (in allele A\*2414).  
 FT VARIANT 121 121 /FTID=VAR\_015765.  
 FT VARIANT 123 123 M -> R (in allele A\*2414).  
 FT VARIANT 123 123 /FTID=VAR\_015766.  
 FT VARIANT 131 131 F -> Y (in allele A\*2414).  
 FT VARIANT 131 131 /FTID=VAR\_015767.  
 FT VARIANT 180 180 G -> W (in allele A\*2414).  
 FT VARIANT 180 180 /FTID=VAR\_015768.  
 FT VARIANT 180 180 Q -> L (in allele A\*2413).  
 FT VARIANT 180 180 /FTID=VAR\_015769.  
 FT VARIANT 187 187 Q -> W (in allele A\*2406).  
 FT VARIANT 187 187 /FTID=VAR\_004358.  
 FT VARIANT 190 191 T -> R (in allele A\*2410).  
 FT VARIANT 190 191 /FTID=VAR\_015770.  
 FT VARIANT 190 191 DG -> EW (in allele A\*2403 and allele  
 FT A\*2410).  
 FT VARIANT 206 206 /FTID=VAR\_004359.  
 FT VARIANT 206 206 T -> A (in allele A\*2401).  
 FT VARIANT 365 AA; 40688 MW; D33684D128F9BEC3 CRC64;  
 SQ SEQUENCE 365 AA; 40688 MW; D33684D128F9BEC3 CRC64;

Query Match 16.1%; Score 44; DB 1; Length 365;  
 Best Local Similarity 100.0%; Pred. No. 3.9e-38;  
 Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 224 QTQDTLTVTRPAGDGTFOKWAIVVPSGEEORYTCHVQHEGLP 267  
 Db 248 QTQDTLTVTRPAGDGTFOKWAIVVPSGEEORYTCHVQHEGLP 291

## RESULT 13

1A30\_HUMAN  
 ID 1A30\_HUMAN STANDARD; PRT; 365 AA.  
 AC P16188; O19598; O62921; P30452; Q9UIP7;  
 DT 01-APR-1990 (Rel. 14, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)

10-OCT-2003 (Rel. 42, Last annotation update)  
 HLA class I histocompatibility antigen, A\*30 alpha chain precursor  
 (MHC class I antigen A\*30).  
 HLA-A OR HLA-A.  
 Homo sapiens (Human).  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 NCBI\_TaxID=9606;  
 [1]  
 SEQUENCE FROM N.A. (A\*3001).  
 MEDLINE=90038496; PubMed=2478623;  
 Kato K., Trapani J.A., Allopenna J., Dupont B., Yang S.Y.;  
 "Molecular analysis of the serologically defined HLA-Aw19 antigens. A  
 genetically distinct family of HLA-A antigens comprising A29, A31,  
 A32, and Aw33, but probably not A30.";  
 J. Immunol. 143:3371-3378(1989).  
 [2]  
 SEQUENCE FROM N.A. (A\*3001).  
 MEDLINE=95176329; PubMed=7871528;  
 Olerup O., Daniels T.J., Baxter-Lowe L.;  
 "Correct sequence of the A\*3001 allele obtained by PCR-SSP typing and  
 automated nucleotide sequencing.";  
 Tissue Antigens 44:265-267(1994).  
 [3]  
 SEQUENCE FROM N.A. (A\*3002).  
 MEDLINE=93056508; PubMed=1431115;  
 Madrigal J.A., Belich M.P., Hildebrand W.H., Benjamin R.J.,  
 Little A.-M., Zemmour J., Ennis P.D., Ward F.E., Petzl-Erler M.L.,  
 Martell R.W., du Toit E.D., Parham P.;  
 "Distinctive HLA-A,B antigens of black populations formed by  
 interallelic conversion.";  
 J. Immunol. 149:3411-3415(1992).  
 [4]  
 SEQUENCE OF 25-279 FROM N.A. (A\*3003).  
 MEDLINE=93209813; PubMed=8458735;  
 Choo S.Y., Starling G.C., Anasetti C., Hansen J.A.;  
 "Selection of an unrelated donor for marrow transplantation  
 facilitated by the molecular characterization of a novel HLA-A  
 allele.";  
 Hum. Immunol. 36:20-26(1993).  
 [5]  
 SEQUENCE FROM N.A. (A\*3004).  
 MEDLINE=96058597; PubMed=8522453;  
 Krausa P., Caracci C., Orru S., Bodmer J.G., Browning M.J., Contu L.;  
 "Defining the allelic variants of HLA-A30 in the Sardinian population  
 using amplification refractory mutation system -- polymerase chain  
 reaction.";  
 Hum. Immunol. 44:35-42(1995).  
 [6]  
 SEQUENCE OF 26-206 FROM N.A. (A\*3004).  
 MEDLINE=96435464; PubMed=8838350;  
 Liener K., Russ G., Bennett G., Gao X., McCluskey J.;  
 "HLA-A\*3004: a new A30 allele identified in an Australian Caucasian  
 population.";  
 Tissue Antigens 46:394-397(1995).  
 [7]  
 SEQUENCE OF 28-205 FROM N.A. (A\*3004).  
 MEDLINE=96124443; PubMed=8560452;  
 Blasczyk R., Wehling J., Paessler M., Hahn U., Hahn D., Salama A.;  
 "A novel HLA-A\*30 allele (A\*3004) identified by single-strand  
 conformation polymorphism analysis and confirmed by solid-phase  
 sequencing.";  
 Tissue Antigens 46:322-326(1995).  
 [8]  
 SEQUENCE OF 26-206 FROM N.A. (A\*3006).  
 MEDLINE=20548605; PubMed=11098929;  
 Ellis J.M., Mack S.J., Leke R.F.G., Quakyi I., Johnson A.H.,  
 Hurley C.K.;  
 "Diversity is demonstrated in class I HLA-A and HLA-B alleles in  
 Cameroon, Africa: description of HLA-A\*03012, \*2612, \*3006 and HLA-  
 B\*1403, \*4016, \*4703.";  
 Tissue Antigens 56:291-302(2000).  
 [9]

SEQUENCE OF 26-206 FROM N.A. (A\*3007).  
 MEDLINE=20309230; PubMed=10852390;  
 Ellis J., Steiner N.K., Kosman C., Henson V., Mitton W., Koester R.,  
 Ng J., Hartzman R.J., Hurley C.K.;  
 "Seventeen more novel HLA-A locus alleles.";  
 Tissue Antigens 55:369-373(2000).  
 [10]  
 SEQUENCE FROM N.A. (A\*3008).  
 MEDLINE=21108617; PubMed=1169261;  
 Cox S.T., McWhinnie A.J., Koester R.P., Heine U., Holman R.,  
 Madrigal A.J., Little A.-M.;  
 "Further diversity at HLA-A and -B loci identified in Afro-Caribbean  
 potential bone marrow donors.";  
 Tissue Antigens 57:70-72(2001).  
 CC -!- FUNCTION: Involved in the presentation of foreign antigens to  
 the immune system.  
 CC -!- SUBUNIT: Heterodimer of an alpha chain and a beta chain (beta-2-  
 microglobulin).  
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -!- POLYMORPHISM: The following alleles of A-30 are known: A\*3001  
 (A30.3), A\*3002, A\*3003, A\*3004 (A30W7), A\*3006, A\*3007 and  
 A\*3008. The sequence shown is that of A\*3001.  
 CC -----  
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 CC -----  
 EMBL; M30576; AAA59612.1; -  
 EMBL; U07234; AAA70162.1; -  
 EMBL; X61702; AAA43871.1; -  
 EMBL; M93657; AAA58650.1; -  
 EMBL; Z34921; CAA84401.1; -  
 EMBL; U19734; AAB53658.1; -  
 EMBL; U18988; AAB53658.1; JOINED.  
 EMBL; U24261; AAB50434.1; -  
 EMBL; X83770; CAA58723.1; -  
 EMBL; X83771; CAA58724.1; -  
 EMBL; AF028714; AAC14191.1; -  
 EMBL; AF028713; AAC14191.1; JOINED.  
 EMBL; AF065643; AAC18600.1; -  
 EMBL; AF065642; AAC18600.1; JOINED.  
 EMBL; AJ249308; CAB57306.1; -  
 EMBL; AJ249309; CAB57306.1; JOINED.  
 EMBL; AJ249310; CAB57306.1; JOINED.  
 EMBL; AJ249311; CAB57306.1; JOINED.  
 EMBL; AJ249312; CAB57306.1; JOINED.  
 EMBL; AJ249313; CAB57306.1; JOINED.  
 EMBL; AJ249314; CAB57306.1; JOINED.  
 EMBL; AJ249315; CAB57306.1; JOINED.  
 PIR; I38519; I38519.  
 PIR; I56039; I56039.  
 DR HSSP; Q95352; IHHK.  
 DR Genew; HGNC:4931; HLA-A.  
 DR MIM; 142800; -  
 DR GO; GO:0005887; C:integral to plasma membrane; NAS.  
 DR GO; GO:0030106; F:MHC class I receptor activity; NAS.  
 DR GO; GO:0006955; P:immune response; NAS.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003597; Ig-cl.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR01039; MHC\_I.  
 DR Pfam; PF00047; ig; 1.  
 DR Pfam; PF0129; MHC\_I\_1.  
 DR PRINTS; PRO1638; MHCCLASSI.  
 DR ProDom; PD000050; MHC-I; 1.  
 DR SMART; SM00407; IGcl; 1.  
 DR PROSITE; PS50835; IG LIKE; 1.  
 DR PROSITE; PS00290; IG\_MHC; 1.  
 DR MHC\_I; Transmembrane, Glycoprotein, Signal, Polymorphism.  
 KW



RESULT 15  
1C02 HUMAN STANDARD; PRT; 366 AA.  
AC P30501; P30502;  
DT 01-APR-1993 (Rel. 25, Created)  
DT 01-APR-1993 (Rel. 25, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE HLA class I histocompatibility antigen, Cw-2 alpha chain precursor  
DE (MHC class I antigen Cw\*2).  
GN HLA-C OR HLA-C.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID:9606;  
RN [1]  
RP SEQUENCE FROM N.A. (Cw\*0201).  
RX MEDLINE=89215297; PubMed=2708822;  
RA Ellis S.A., Strachan T., Palmer M.S., McMichael A.J.;  
RT "Complete nucleotide sequence of a unique HLA class I C locus product  
expressed on the human choriocarcinoma cell line BeWo.";  
RL J. Immunol. 142:3281-3285(1989).  
RN [2]  
RP SEQUENCE FROM N.A. (Cw\*0202).  
RX MEDLINE=89235215; PubMed=2715640;  
RA Farham P., Lawlor D.A., Lomen C.E., Ennis P.D.;  
RT "Diversity and diversification of HLA-A,B,C alleles.";  
RL J. Immunol. 142:3937-3950(1989).  
CC -!- FUNCTION: Involved in the presentation of foreign antigens to the  
immune system.  
CC -!- SUBUNIT: Heterodimer of an alpha chain and a beta chain (beta-2-  
microglobulin).  
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -!- POLYMORPHISM: The following alleles of Cw-2 are known: Cw\*0201  
(Cw2.1) and Cw\*0202 (Cw2.2). The sequence shown is that of  
Cw\*0201.  
CC  
CC  
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CC  
CC  
CC EMBL; M26430; AA59703.1; -.  
CC EMBL; M24030; AA59671.1; -.  
CC PIR; I61866; I61866.  
CC HSSP; P30685; 1A9E.  
CC Genew; HGNC:4933; HLA-C.  
CC MIM; 142840; -.  
CC GO; GO:0005887; C: integral to plasma membrane; NAS.  
CC GO; GO:0030106; F: MHC class I receptor activity; NAS.  
CC GO; GO:006955; P: immune response; NAS.  
CC InterPro; IPR007110; Ig-like.  
CC InterPro; IPR003597; Ig cl.  
CC InterPro; IPR003086; Ig\_MHC.  
CC InterPro; IPR001039; MHC\_I.  
CC Pfam; PF00047; Ig; 1.  
CC Pfam; PF00129; MHC I; 1.  
CC PRINTS; PR01638; MHCCLASSI.  
CC ProDom; PD000050; MHC I; 1.  
CC SMART; SM00407; IGcl; 1.  
CC PROSITE; PS00835; IG\_LIKE; 1.  
CC PROSITE; PS00290; IG\_MHC; 1.  
KW MHC I; Transmembrane; Glycoprotein; Signal; Polymorphism.  
FT SIGNAL 1 24  
FT CHAIN 25 366 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,  
FT CW-2 ALPHA CHAIN.  
FT DOMAIN 25 114 EXTRACELLULAR ALPHA-1.  
FT DOMAIN 115 206 EXTRACELLULAR ALPHA-2.  
FT DOMAIN 207 298 EXTRACELLULAR ALPHA-3.  
FT DOMAIN 299 308 CONNECTING PEPTIDE.

TRANSMEM 309 333  
CYTOPLASMIC TAIL.  
FT DOMAIN 334 366 BY SIMILARITY.  
FT DISULFID 125 188 BY SIMILARITY.  
FT DISULFID 227 283 N-LINKED (GLCNAC. .) (BY SIMILARITY).  
FT CARBOHYD 110 110 E -> A (in allele Cw\*0202).  
FT VARIANT 5 5 /FTID=VAR\_016556.  
FT VARIANT 10 10 I -> L (in allele Cw\*0202).  
FT VARIANT 73 74 GR -> AP (in allele Cw\*0202).  
FT VARIANT 92 92 /FTID=VAR\_016558.  
FT VARIANT 179 179 N -> K (in allele Cw\*0202).  
FT VARIANT 202 202 E -> Q (in allele Cw\*0202).  
FT VARIANT 364 364 /FTID=VAR\_016560.  
FT VARIANT 366 AA; 41095 MW; AD8025DEB7DA8CE6 CRC64; /FTID=VAR\_016561.  
FT SEQUENCE 366 AA; 41095 MW; AD8025DEB7DA8CE6 CRC64; /FTID=VAR\_016562.  
Query Match 16.1%; Score 44; DB 1; Length 366;  
Best Local Similarity 100.0%; Pred. No. 3.9e-38;  
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Cv 224 QTQDTVELTRPACDGTGTFQKWAADVPSGEQRYTCHVQHEGLP 267  
Db 248 QTQDTVELTRPACDGTGTFQKWAADVPSGEQRYTCHVQHEGLP 291  
Search completed: June 18, 2004, 19:30:22  
Job time : 17 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 18, 2004, 19:28:12 ; Search time 20 Seconds  
(without alignments)  
1317.824 Million cell updates/sec

Title: US-09-819-371-5  
Perfect score: 274  
Sequence: 1 GSHSLRFTAVSRPGRGEP.....QRYTCHVQHEGLPQLILRW 274

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 283366 seqs, 96191526 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : PIR 78:\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	274	100.0	362	2 A60384	MHC class I histoc
2	126	46.0	345	2 S07114	MHC class I histoc
3	73	28.6	316	2 C37028	MHC class I histoc
4	59	21.5	348	2 S29990	histocompatibility
5	44	16.1	275	1 HLH10	MHC class I histoc
6	44	16.1	298	2 S44994	class I histocompa
7	44	16.1	313	2 I36958	MHC class I histoc
8	44	16.1	325	2 I54449	MHC class I histoc
9	44	16.1	332	2 S06424	MHC class I histoc
10	44	16.1	345	2 I68749	MHC class I lympho
11	44	16.1	354	2 I54551	histocompatibility
12	44	16.1	357	2 I36966	MHC class I protei
13	44	16.1	357	2 I36965	MHC class I histoc
14	44	16.1	359	1 HLH12	MHC class I histoc
15	44	16.1	364	2 S03535	class I histocompa
16	44	16.1	365	2 S77963	MHC class I histoc
17	44	16.1	365	2 I37476	MHC class I histoc
18	44	16.1	365	2 I37478	MHC class I histoc
19	44	16.1	365	2 S01171	class I histocompa
20	44	16.1	365	2 A47636	MHC class I histoc
21	44	16.1	365	2 I61856	MHC class I histoc
22	44	16.1	365	2 I83063	Al1.2 - human
23	44	16.1	365	2 I36961	MHC class I protei
24	44	16.1	365	2 I54416	HLA-A*24 protein
25	44	16.1	365	2 I38519	MHC class I histoc
26	44	16.1	365	2 I56039	HLA-A*30.3 precu
27	44	16.1	365	2 I54493	MHC class I histoc
28	44	16.1	365	2 I38518	HLA-A*0102 allele
29	44	16.1	366	1 HLH0W3	MHC class I histoc

30	44	16.1	366	2 JS0262	class I histocompa
31	44	16.1	366	2 B37028	MHC class I histoc
32	44	16.1	366	2 S42823	MHC class I histoc
33	44	16.1	366	2 I37523	MHC class I histoc
34	44	16.1	366	2 JH0526	MHC class I histoc
35	44	16.1	366	2 I37527	MHC class I histoc
36	44	16.1	366	2 I72113	MHC histocompatibi
37	44	16.1	366	2 I38507	MHC class I histoc
38	44	16.1	366	2 I37526	MHC class I histoc
39	44	16.1	366	2 I61866	MHC class I histoc
40	44	16.1	366	2 I38505	MHC class I histoc
41	44	16.1	366	2 I68712	MHC class I histoc
42	44	16.1	366	2 I81231	lymphocyte antigen
43	44	16.1	366	2 I81232	lymphocyte antigen
44	44	16.1	366	2 I37544	MHC class I histoc
45	44	16.1	366	2 I37135	MHC class I histoc

ALIGNMENTS

RESULT 1

A60384  
MHC class I histocompatibility antigen HLA-F alpha chain Dew3 precursor - human  
C:Species: Homo sapiens (man)  
C:Date: 03-Mar-1993 #sequence\_revision 03-Mar-1993 #text\_change 23-Jul-1999  
C:Accession: A60384; JI0147  
R:Lury, D.; Epstein, H.; Holmes, N.  
Int. Immunol. 2, 531-537, 1990  
A:Title: The human class I MHC gene HLA-F is expressed in lymphocytes.  
A:Reference number: A60384; MUID:91197899; PMID:1707859  
A:Accession: A60384  
A:Molecule type: DNA  
A:Residues: 1-362 <LUR>  
R:Graghty, D.E.; Wei, X.; Orr, H.T.; Koller, B.H.  
J. Exp. Med. 171, 1-18, 1990  
A:Title: Human leukocyte antigen F (HLA-F): an expressed HLA gene composed of a class I  
A:Reference number: JI0147; MUID:9011605; PMID:1688605  
A:Accession: JI0147  
A:Molecule type: DNA  
A:Residues: 1-362 <GER>  
A:Cross-references: GB:X17093; NID:G32223; PIDN:CAA34947.1; PID:G312407  
A:Experimental source: Lymphoblastoid cell line  
C:Genetics:  
A:Gene: GDB:HLA-F  
A:Cross-references: GDB:125714  
A:Map position: 6p21.3-6p21.3  
A:Introns: 22/1; 112/1; 204/1; 296/1; 335/1; 346/1; 362/1  
C:Superfamily: class I histocompatibility antigen; immunoglobulin homology  
C:Keywords: Glycoprotein; heterodimer; transmembrane protein  
F:1-21/Domain: signal sequence #status predicted <SIG>  
F:22-111/Domain: alpha-1 <All>  
F:78-104/Region: hypervariable  
F:112-203/Domain: alpha-2 <AL2>  
F:164-192/Region: hypervariable  
F:204-295/Domain: alpha-3 <AL3>  
F:217-282/Domain: immunoglobulin homology <IMW>  
F:107/Binding site: carbohydrate (Asn) #status predicted

Query Match 100.0%; Score 274; DB 2; Length 362;  
Best Local Similarity 100.0%; Pred. No. 5.3e-282;  
Matches 274; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	GSHSLRFTAVSRPGRGEPRIAYEVDDTQFLRSDDAIIRMEPRPWEQEGPOYW	60
Db	22	GSHSLRFTAVSRPGRGEPRIAYEVDDTQFLRSDDAIIRMEPRPWEQEGPOYW	81
Qy	61	EWTTGYKANAQTRVALRNLRLRYNOSEAGSHTLQMGNGCDMGDPGRLLRGVHQHAYDG	120
Db	82	EWTTGYKANAQTRVALRNLRLRYNOSEAGSHTLQMGNGCDMGDPGRLLRGVHQHAYDG	141
Qy	121	KDYISLNEDLRSWTAADTVAQITQRFVYEAEEFTYLEGECLELLRRLYLENGKETLQ	180